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February 12, 2003, 22:31:05 ; Search time 3253 Seconds (without alignments) 286.286 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4109280
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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32
1 taatacaacacaatattaattgtgttgtatta 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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em_htgo_mus:*
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                                                                                                                                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a

cereus group.

1 (bases 1 to 4149)
Mahillon,J. and Lereclus,D.
Structural and functional analysis of Tn4430: identification of an integrase-like protein involved in the co-integrate-resolution

REFERENCE AUTHORS TITLE

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			SOMMAKLES		
Result		Query					
No.	Score	Match	Length	DB		scriptio	
1		100.0	4149	1	BTTN4430		
(2)		100.0	9672		BTPGI2XX	X13481 Bacilli	
	S	80.0	4149		BTTN4430	X07651 Bacill	
O 4	25.6	80.0			BTPG12XX	X13481 Bacillus	is th
	4 -	76.9	164303		AC027541	AC027541 Homo	sapi
7	23	2.07	∽ α	7 -	AC100807	AC100807 Homo	sapi
ω υ	23	71.9	94535	`	AC083886		
	23	71.9	-		AC003028	AC003028 ACAB	Sapi
	23	71.9			AL161631	AL161631 Human	S AND
c 11	53	71.9	α		AC017792	AC017792 Drose	Drosoph11
	23	71.9	マ L		AC011096	AC011096 Homo	sapi
	22	71.9	n v		AC084188	AC084188 Homo	Sapi
	23	71.9	2 6		AC008254	AC008254 Drose	phil
c 16		71.9	· 0		AC068896	ACOUSTS Drosophil	phil
•		70.6	0		HSJ324N14		Sapi
		9.07	10		AC025996	E CH	sant
		70.6	~ 1		AL845419	Dan	rer
•		70.0	\ 0		AC034140	HOM	sapi
0 25		70.6	198742		AC121330 A1355360	HOH	Sapi
•		70.0			MISCARS	E to	sapı +DN3
24		70.0	929		YSCMTAP92	J01461 Yeast	S.ce
25		70.0	606		MISC28	X00818 Yeast m	itoc
270		0.0			YSCMTCG16	L36900 Sacchar	omyc
28		0.0			AYU820/0	AY082070 Bacte	riop
29	22.4	70.0	91061		AC087139	AJULI856 Saccharom	arom
c 30			'n		AC116976	ACUS/139 MUS II AC116976 Dictv	uscu
31	22.4				AC009886	AC009886 HOMO	sapi
32.6	22.4		9		AL357672	AL357672 Human	DNA
, (*)	22.4		~ ~		AC113127	AC113127 Mus muscu	nsen
35	22.4		. ~		AC113106	g G	s no
c 36	22.4		8		AC109717	11.5 H	muscu
m	22.4		8		AC026124	Jomo L	Sapi
38 0	22.4		æ.		AC068643	OHO	Sapi
T) 4	22.4		<u> </u>		AC025580	lomo	Sapi
7 -	4.72				AC121884	lus n	muscu
* 4			7 5		HSXDPB	5	sapi
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45	22	68.89	150587		AC007549	ACIDELYO KATTU ACO07549 Droso	tus no
						•	1
					ALIGNMENTS		
RESULT 1							
BTTN4430		0647					
DEFINITION	z		thuringiens	•~	4149 bp L s transposon Tn	DNA linear BCT 12-SEP Tn4430.	9-1993
VERSION VERSION			GT:40347				
KEYWORDS		plasmid; re	resolvase	:: ::	tnpA gene; tnpI	gene; transposase; transposon	oson.
ORGANISM		llus th	thuringiensis	nsis	w w		
	Bact	eria; E	irmicut	es;	Bacillales;	Bacillaceae; Bacillus; Bacillus	lus
	cereus	us group	.d)

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plasmid; plasmid pG12; recombinase; resolvase; transposase;
                                                                                                                                                                                                                                                                                                                Mahillon, J.
Direct Submission
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JOURNAL
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X13481.
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PTLLRSLHFRATKSGEPVLQALDTHELWERGKRYPYGAPLHFVSRRWOKHVYDDG
NRRHYYELAALTELNHIRSODIFTOSGRHRAFDDYLIPYDEWNEVSNIPWGLTAP
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INRRHYTELLATIOHNELLEWLSKNERKLEGYDISGRHYENDGTTAP
INSMLPRIKLTDLLIEVASWRTGFHQQFILMSTNUNGTHY
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TDLKIEEHYTDTAGYTDQVPALTHLIGFREARIRDLADVELSIRGGEEYENVQALL
KRINNKLIRENYEDIRRLAYSVQTGKVSSALIMGKLGSYARONKLATALGEMGRIEK
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VVNRIFKSYSNVITPHQLRHFFCTNAIEKGFSIHEVANQAGHSNIHTTLXTNPNQLÖ
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                                                                                                       Data kindly reviewed (03-APR-1989) by Lereclus D.
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/note="transposase Tnp A (AA 1 - 987)"
                                                                                                                                                  1. .4149
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776 q 1182
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EMBO J. 7 (5), 1515-1526 (1988)
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TLIEARETGKDARALDEVMSNNEMVESVEEAKQLSRPLNYDYLDLINTRYSYVRRY
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MARATPGISTROMANNSQWRYDDAWWRAQSILVWFOKEGKSSYWGGTISSSGMR
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TDLK EEHYTDTAGYTDQVFALTHLLGFRFAPRIRDLADTKLFSIPGGEEYENVQALL
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TLFTLDYISNKAVRRRVQKGLNKGEAINALARTIFFGQRGEFRERALQDQLQRASALN
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TGECIIRSGKGGKORTVLLASKVLSAIKDYLIDRKTYSTAHESPYLEISKKREKLDRY
VVNRIFKSYSNVITPHQLRHFFCTNAIEKGFSIHEVANQAGHSNIHTTLLYTNPNOLO
transposon; unidentified reading frame.
Bacillus thuringiensis.
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                        1 (bases 1 to 6999)
Mahillon, J. and Seurinck, J.
Complete nucleotide sequence of pG12, a Bacillus thuringiensis plasmid containing T104430
Nucleic Acids Res 16 (24), 11827-11828 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-NOV-1988) Mahillon J., Plant Genetics Systems, J Plateaustraat 22, B-9000 Gent, Belgium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Bacillus thuringiensis"
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/note="inverted repeat A"
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493 .497
/note="direct repeat 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .4580
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3 (bases 1 to 9672)
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247. .1101
/note="put. resolvase Tnp I (AA 1 - 284)"
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/note="transposase Tnp A (AA 1 - 987)"
                                                                                                                                                                                                                                      kindly reviewed (03-APR-1989) by Lereclus
                                                                                                                                                                                                                                                                                             /organism⇒"Bacillus thuringiensis"
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685 c 776 q 1182 t
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Pred. No. 49;
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88312602
2842151
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                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="pBR322"
                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        /map="plasmid pGI2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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      Bacillus thuringiensis.
Bacillus thuringiensis
Bacteria; Firmicutes; E
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87.5%;
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                                                                cereus group
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Best Local Similarity
Matches 28; Conserv
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    SOURCE
ORGANISM
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ORIGIN
                                                                                REFERENCE
                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVTPRGSWGGFTLKAGDIFITNATSSAGIVGHAAIANGDNYILHMPGAGOGNOOLSTS
NWMQKYTASGKWIKVYRLKDQTLARDVARYADRNFYSTTGSATKNVYLDYGIDTHLYO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDLINQOKIRYESTIKQEISERVKRKPRANSYVLSERVYTASPDYMHSLSLEEGKRYF
ESSLDFIGKRYGKONTLYAMVHMDEATPHMHIGYMPITEDNRLSAKDMFTRKELISLQ
QDFPLEMREKGFDVDRGEGSEKKHLSPQAFKEKQDLEVEVEQLSNVKTHLKTKVVFTH
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TKTEVTTKLFGKPEITEKKTGNI VVTREQMRDMTEKVNAAV I VKKDY ERLOKTDLVKE
NQSLREDNKYLEETIKGNNLALKHSYKQNRELEEVNKELHTEIGTLKAHI RDLQMNI K
IIINAISVWNTVYMEKAVEELKARGEFREDLMPYAWPLGWEHINFLGEYKFEGLHDTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLYQQTKKVFKEQFKAFRGLIKNELDMKGVDNQFEREHTREIRSRQKGYDMER"
1419 c 1788 q 2891 t
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0
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; Pred. No. 0.32;
0; Mismatches 0; Indels
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Bacillus thuringlensis transposon Tn4430.
X07651
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                                      4609. .4646
/note="inverted repeat A'"
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                                                                      4647. .4651
/note="direct repeat 1"
4859. .5473
/note="ORF 1"
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nes 32; Conserv
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plasmid;
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                                                                            repeat_region
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BTTN4430/c
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MOVAKQFSSYLKQBNKTENTVOGYTSGIRQYIKWFGGSVDRKLT
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VVNRIFKSYSNVITPHOLRHPFCTNAIEKGFSIHEVANQAGHSNIHTLLYTNNDQLQ
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LSTAYRSLHADSNPHYGTGKGGTIXFRYSDOLSAYHYKVTTHARDALHHYDGCLHHB
TDLKIEEHYTDTAGYTOQYPALTHLIGFRFARRIRDLADTKLFSIPGGEEYENVOALL
KGKINVKLIKENYEDIRRLAYSVQTGKVSSALIMGKLGSYARQNKLATALGEMGRIEK
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IIINAISVWNTVYMEKAVEELKARGEFREDLMPYAWPLGWEHINFLGEYKFEGLHDTG
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                                                                                                                                                                                    ឧប
Bacillales; Bacillaceae; Bacillus; Bacillus
                                                                                1 (bases 1 to 4149)
Mahlllon, J. and Lereclus, D.
Structural and functional analysis of Tn4430: identification of
integrase-like protein involved in the co-integrate-resolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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NINRHYYELAALTELRNHIRSGDIFVSGSRHHKAFDDYLIPYDEWNEVSNIPNGLTAP

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BTPGI2XX 9672 bp DNA linear BCT 07-JUL-2002 Bacillus thuringiensis plasmid pG12 with transposon Tn4430.
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/translation="MDVAKQFSSY1KQENKTENTVQGYTSGIRQYIKWFEGSYDRKLT
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OTVYASPTOIVELDVKKFLOSVLEDNNKNYAIATLLAYTGVRISEALSIKMNDFNLQ
TGECIIRSGKGGKORIVLLNSKVLSAIKDYLIDRKTYSTAHESPYLFISKKREKLDRT
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RGYNRLGFALRLVLIRYPGWSLTEYKDIPQYVVAYVTSRLRIPPEEFLVYAKRGNTLW
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YVIEDIVWEAKQQADQKVYSILHDGLVQEQKDQLDALLLPTJNGKSPLAWLKDVPAQP
SPESFLKVJDRLQFVQKIGLTJDTTKINTNRLRQLARLGSKYEPYAFRRFNEVKRYSM
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TLIEAKETGKDAFAALDEVMSWNEMVESVEEAKQLSRPLNYDYLDLLNTRYSYVRRYA
PTLLRSLHFRATKSGEPVLQALDTIHELNETGKRKVPHGAPLHFVSNRWQKHVYDDDG
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                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
                                                                                                                                                                                                                                         cereus group.

1 (bases 1 to 6999)

Mahillon, J. and Seurinck, J.
Complete nucleotide sequence of pGI2, a Bacillus thuringiensis plasmid containing Tn4430
Nucleic Acids Res. 16 (24), 11827-11828 (1988)
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Submitted (04-NOV-1988) Mahillon J., Plant Genetics Systems,
Plateaustraat 22, B-9000 Gent, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission 20 Mark-1998) Hoflack L., Plant Genetics Systems, Plateaustraat 22, B-9000 Gent, Belgium on July 2, 1998 this sequence version replaced gi:40316.
                                                                                                                                            recombinase; resolvase; transposase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .9672
/organism="Bacillus thuringiensis"
/Astrain="thuringiensis H1.1."
/db_xref="taxon:1428"
/plasmid="pG12"
                                                                                                                                                               transposon; unidentified reading frame. Bacillus thuringiensis.
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/codon_start=1
/transl_table=11
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/note="inverted repeat A"
744. .1598
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/protein_id="CAA31832.1"
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/note="direct repeat 1"
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/transposon="Tn4430"
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                                                                                                                                            plasmid; plasmid pGI2;
                                                                                                                                                                                                                Bacillus thuringiensis
                                                                                                                 X13481.1 GI:3171732
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Hoflack, L.
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RESULT 4
BTPGI2XX/c
                                                                  DEFINITION
                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
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AUTHORS
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                                                                                                                                            KEYWORDS
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DONGYSYNEWILKONNEEFMPTYQDGIKOGYPLEPLSYNEWIKLINNYGQAPTGDTELFD
DYTPRGSWGGFTLKAACDIFTTNATSSAGIYGHAAIANGDNYILHMPGAGQGNQQLSTS
NWMQKYTASGKWIKYYRLKDQTLARDVARYADRNFYSTTGSATKNYYLDYGIDTHLYQ
KNPTYCSKLYFQALYFGSGSRNVMQAVSGIYTPYGLIDTFTSAYRPSLVKTY
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NQLQQTTNYIEKQNETLOKIQOQFLSLDKKIKEKKOEFETFRNQIPDKPVSMSYLREE
TKTEVTTKLECKPEITEKKTGNIVYPREQWRDMTEKVNAAVIVKRDYERLOKTEDLYK
NQSLREDWYKLEETIKGNNLALKHSYKONRELEEVNKELHTEIGTLKAHIRDLOMNIK
VLYQQYRKVFKEQFRARGLIKNELDMKGVDNQFEREHTREIRSRQKGYDMER*
1119 c 1788 g 2891 t
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ESSLDFIQKRYGKQNTLYAMVHMDEATPHMHIGVMPITEDNRLSAKDMFTRKELISLQ
                                                                                  MAEATPGISYRQMANASQWRMYDDAMYRAQSILVNFQKEQKLSSYWGDGTTSSSDGMR
LSIAVRSLHADSNPHYGTGKGGTIYRFVSDQLSAYHVKVITTNARDALHVLDGLLHHE
TDLKIEEHYTDTAGYTDQVFALTHLLGFRFAPRIRDLADTKLFSIPGGEEYENVQALL
                                                                                                                                                                                                              KGKINVKLIKENYEDIRRLAYSVOTGKVSSALIMGKLGSYARONKLATALGEMGRIEK
TLFTLDYISNKAVRRRVQKGLNKGEAINALARTIFFGQRGEFRERALQDQLQRASALN
IIINAISVWNTVYMEKAVEELKARGEFREDLMPYAWPLGWEHINFLGEYKFEGLHDTG
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/translation="WINTIDEKHVERNARIRDFENEKEKFKODHNGINGEEVNOAMOV
/translation="Wintidek"
//db_xref="Wintidek"
//db_x
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LKAEDYITDRINRLNEHLEWLSKNSEKLEGVDISQGKLHVERLDRGTPEEAKAFSKLL
HSMLPRIKLTDLLIEVASWTGFHDQFIHASTNQSPDQEEQNIVLATLMAMGTNIGLTK
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/protein_id="CAA31835.1"
/db_xref="GI:40322"
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/db_xref="SMISS-PROT:P10023"
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Pred. No. 40;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  OMNLRPLRIKEPFYS"
4609. .4646
/note="inverted repeat A'"
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/db_xref="GI:3171733"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4647. .4651
/note="direct repeat 1"
4859. .5473
/note="ORF 1"
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/transl_table=11
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/note="ORF 2"
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87.5%;
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Best Local Similarity
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AC100807
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KEYWORDS
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                                                                 HTG 17-AUG-2002
                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                      AC027541 11near Homo sapiens chromosome 8 clone RP11-324F11 map 8, IN PROGRESS ***, 1 ordered piece.
                                                                                                                                                   AC027541.11 GI:22296720
HTG: HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                          1 (bases 1 to 164303)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-324F11
                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                    AC027541
                                                                                                                                                                                                             human.
RESULT 5
AC027541/c
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AUTHORS
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Contact: sequence_submissions@genome.wi.mit.edu

Web site: http://www-seq.wi.mit.edu

COMMENT

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Anderson, S., Barna, N., Bastien, V., Bouslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Bouslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Candyna, Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ginde, S., Goyette, M., Graham, L., Garduns, S., Gardyns, S., Goyette, M., Graham, L., Cardun-Pierre, N. Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K., Liu, G., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Morpheeters, R., Liu, G., Maclar, J., Mechan, C., M., O'Donnell, P., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Plerre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riles, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riles, C., Schupback, R., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Tasfaye, S., Theodore, J., Topham, K., Travers, M., Traviglilo, J., Vassiliev, H., Viel, R., Voo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Lainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176759)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the piaces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

I 164303: contig of 164303 bp in length.
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                             NOTE: This is a 'working draft' sequence.
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Homo sapiens chromosome 8, clone CTD-2534J5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 76.9%; Score 24.6; DB 2; 1 Similarity 87.1%; Pred. No. 44; 27; Conservative 0; Mismatches 4;
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               Information
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
Center project Informati
Center project name: L8782
Center clone name: 324_F_11
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AL663040
AL663040.6 GI:18855245
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Best Local Similarity 83.99
Matches 26; Conservative
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AC083886.19
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       Direct Submission

Direct Submission

Direct Submission

Direct Submission

Submitted (22-NoV-2011) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Si (bases 1 to 176759)

Si (bases 1 to 176759)

Saria, N. Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Chopel, Y., Collymore, A., Cooke, P., DeArellano, K., Dear, J., Grand, Pierre, M., Gage, D., Galagan, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Faro, S., Ferreira, P., EitzGerald, M., Gage, D., Galagan, J., Raratas, A., Kells, C., Landers, T., Levine, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Kamat, A., MacLean, C., MacGnahld, P., Major, J., Matthews, C., MacChy, T., Maylor, J., Maylor, J., Maneus, L., Mihova, T., Meldrim, J., Meneus, L., Mihova, T., Melda, V., N., Raymond, C., Retta, R., Rise, C., Rogov, P., Poman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (20-Aug-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Nall repeats were identified using RepeatMasker: html

Http://ftp:genome.washington.edu/RW/RepeatMasker:html

Http://ftp:genome.washington.edu/RW/RepeatMasker:html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
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117263 176759: contig of 59497 bp in length.
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/clone_lib="CITD2 Human BAC"
a 37301 c 35610 g 51038 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
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Center clone name: 2534_J_5
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87.1%;
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AL663040
LOCUS
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ORIGIN
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pearce, A.

Direct Submission

AL Direct Submission

Direct Submission

Direct Submission

Submitted (16-FBB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries:

Cambridgeshire, CBIO 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

During sequence assembly data is compared from overlapping clones

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double stranded above.

This sequence was finished as follows unless otherwise noted: all regions were either double stranded all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL: Sw:, SWISSPROT; TT:, TREMBL: WORMPEP; Information on the WORMPEP their covered by the content of t
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Homo sapiens 3 BAC RP11-364F11 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 81885)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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26614 a 14835 c 14385 g 26051 t
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/db_xref="taxon:10090"
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Naumalia's butheria; Primates; Catarrhini; Hominidae; Homo.

Naury, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabrooks, S.L., Amaratunge, H.C., Aet. J.R., Ayele, M., Banks, T., Barbarla, J., Benton, J., Bingel, K., Blankenburg, K., Bonnin, D. Barbarla, J., Benton, J., Bingel, K., Blankenburg, K., Bonnin, D. Bundy, C., Burch, P., Burkett, C., Burrell, K.L., Davis, C., Burrell, K.L., Davis, C., Burchl, R., Charca, J., Chavez, D., Chavez, D., Chan, G., Chen, R., Carter, M., Cavazos, S.R., Chacko, J. Chavez, D., Chan, G., Chen, R., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davyla, M.L., Davis, C., Burrell, L., Dederlich, D., Avid, R., Davila, M.L., Davis, C., Edwards, C.C., Edwards, C., Edwards, C., Edwards, C., Edwards, C., Edwards, C., Edwards, C., Hand, M., He, X., Harris, K., 
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Direct Submission
Submitted (05-00T-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA
Worley, K.C.
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Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 94535)
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On Jul 26, 2002 this sequence version replaced 91:21952622.
Primates; Catarrhini; Hominidae; Homo.
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gc-help@bcm.tmc.edu
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Unpublished
2 (bases 1 to 94535)
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SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot
                                                                                   Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                      STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
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729
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1365. 1393
/rpt_family="AT_rich"
complement(3179. 3270)
/rpt_family="L2"
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complement(14419. .14672)
/rpt_family="MIR"
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/db_xref="taxon:9606"
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1145. .1277
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5911. 6195
/rpt_family="Alusc"
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5662, .5848
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complement(12092,
/rpt_family="MIR"
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16326. .16354
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ANNOTATION OF FEATURES:
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15660. .15729
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4425. .4494
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                                  Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
3 (bases 1 to 115359)
Town, C.D. and Kaul, S.
Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA, edtownétigr.org
On Apr 18, 2002 this sequence version replaced gi:6598384.
Location/Qualifiers
1. 115359
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Arabidopsis thaliana chromosome 2 clone F16M14 map ve018, complete
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 115359)
Rounsley,S.D., Kaul,S., Lin,X., Ketchum,K.A., Crosby,M.L.,
Brandon,R.C., Sykes,S.M., Mason,T.M., Kerlavage,A.R., Adams,M.D.,
Unpublished
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AC003028
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SOURCE

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Direct Submission

Submitted (15-Nov-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries:

Cambridgeshire, CBIO 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

Nov 16, 2001 this sequence version replaced gi:15072563.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission or variation annotation may not be found in the sequence submission only a small overlapping clone, as we submit sequences with
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microsatellite repeat region (clone 74A)#Rf:ATR0046|x93607
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Human DNA sequence from clone RP11-70K10 on chromosome 9, complete
sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 119819)
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ι.6e+02;
ι.α 5; Indels
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nilarity 83.9%; Pred. No. 1.6e+02
Conservative 0; Mismatches
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                                                                                                                                                                                                                      /note="F16M14.3"

complement(join(<16211. .17060,17144. .17637,17734. .>17955))

/gene="At2g38100"

/gene="At2g38100"

/gene="At2g38100"
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/product="unknown protein"
/protein_id="AAC27160.1"
/db_xref="G1:3335359"
/translation="MAGARRREEDISKCDVKDRSNHTVAADLDGTLLISRSAFPYY
FLVALERGSLIRALILLVSVPFVYLTYLTISFTLAINVFVFTFAGLKIRDVELVVRS
VLPRFYAEDVRPDTWRIFNTFGKRYIITASFRIWYEPFWKFLGYDKVLGTELEVSKS
GRATGFTRKPGILVGOYKRDVVLREGGLASDLPDLGLGDSKTDHDFWSICKEGYWVP
RTKGEPLPRNKLLSPIIFHEGRLVQRRTPLYALLFFLWLPVGFVLSIIRYYTNIPLPE
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YSISKFSELISPIKAVALTRQREKDAANIKRLLEEGDLVICPEGTTCREPFLLRFSAL
FAELTDRIVPVAINTKQSMFNGTTTRGYKLLDPYFAFMNPRPTYETTFLKQIPAELTC
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23124. .23191
/rpt_family="Rf:gi|1100803|emb|X93607.1|AT74A A.thaliana
//rpt_family="Rf:gi|1100803|emb|X93607.1|AT74A A.thaliana
microsatellite repeat region (clone 74A)#Rf:ATR0046|X93607
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microsatellite repeat region (clone 74A)#Rf:ATR0046|X93607
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microsatellite repeat region (clone 74A)#Rf:ATR0046|x93607
                                                                                                                             /product="putative MYB family transcription factor"
/proteIn_id="AAC2119.1"
/db_xref="G1:335378"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGGKSPIEVANTORVLGGTLGFECTNFTRKDYKRAMLAGTDGRVPVKKEKT"
23106. .23191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative peptide/amino acid transporter"
/protein_id="AAC27159.1"
/db_xref="GI:3335358"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(<20543. .21412,22456. .>23154))
/gene="At2g38110"
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/gene="At2g38110"
                         Join(13026. .13450,14052. .14502)
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/gene="At2g38110"
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RESULT 12
AC011096/c
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                                                                                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping croup. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RPI1-70kIO is from the library RPCI-11.1 constructed by the group of pieter de Jong. For further details see http://www.chorl.org/Pacpac/Mome.htm
VBCTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RPI1-70kIO it may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true left end of clone RPI1-35N6 is at 2000 in this sequence. The true right end of clone RPI1-35N6 is at 2000 in this sequence.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 suclone; and the assembly was confirmed by restriction digest The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw.; SWISSPROT; TI., TREMBL; WP., WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC017792 123579 bp DNA linear HTG 09-DEC-1999
Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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Submitted (No. USA
Rockville, MD, USA
This sequence was identified as CDM:10212105 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a "working draft' sequence.
* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 123579)

Adams, M. and Venter, J.C.
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Location/Qualifiers
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Pred. No. 1.6e+02;
0; Mismatches 5; Indels
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/db_xref="taxon:7227"
[ 25889 c 26096 g 35734 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="9"
/clone="RP11-70K10"
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HTG; HTGS_PHASE2.
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71.9%;
Best Local Similarity 83.9%;
Matches 26; Conservative (
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ORIGIN
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AC017792/c
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BASE COUNT

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Dipublished

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Birren, B., Linton, L., Nolangalo, M., Collins, S., Collymore, A., Castle, A., Calangelo, M., Collins, S., Collymore, A., Castle, A., Clangelo, M., Domelan, L., Doyle, M., Ferreira, P., Fizhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehockky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McDwan, P., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Kiley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Lincet Submission

All repeats were identified using RepeatMasker:

Smit, A. F. A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html

Conter: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                         AC011096 145734 bp DNA linear HTG 28-SEP-2000
Homo sapiens clone RP11-2D21, WORKING DRAFT SEQUENCE, 4 unordered
                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a working draft, sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               web size: nict;//www.seq.willit.euu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Conter project Information
Center project name: 11511
Center clone name: 2_D_21
Center clone name: 2_D_21
Center clone name: 2_D_21
Center clone page: 2_D_21
Center clone page: 2_D_21
Center clone page: 2_D_21
Center clone page: 2_D_21
Center clone plasmid; n/a; 7% of reads
Chemistry: Dye-terminator Big Dye; 97% of reads
Chemistry: Dye-terminator Big Dye; 97% of reads
Chemistry: Dye-terminator Big Dye; 97% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 14534 bases at least Q30
Consensus quality: 145434 bases at least Q20
Insert size: 150000; agarose-fontigs
Onality coverage: 77 in Q20 bases: a
                                                                          ..
       Length 123579;
                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Homi
1 (bases 1 to 145734)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-2D21
Score 23; DB 2; Le
Pred. No. 1.6e+02;
0; Mismatches 5;
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                                                                                                                                                                                                DD 36974 AACAAAAGACAATATTAATTGTGTTATTTA 36944
                                                                                                                                                             2 AATACAACACAATATTAATTGTGTTGTATTA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC011096
AC011096.3 GI:10334908
HTG; HTGS_PHASE1; HTGS_DRAFT.
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           71.9%;
83.9%;
                                                                                      Conservative
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   Query Match
Best Local Similarity
Matches 26; Conserv
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58646 58745: gap of 100 bp
58746 61720: contig of 2975 bp in length
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                                                                                                                                                Direct Submission
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35624
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4033
5774
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33635
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barra, N., Bastlen, V., Bedaf, F., Boguslavkly, L., Boukhqaiter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dewrark, Dewark, Daz, J.S., Dodge, S., Ferreira, P., FitzHugh, W. Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grand Plerre, N., Hagos, B., Heaford, A., Horton, L., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, M., Moczarthy, M., McEwan, P., McKernan, K., Morrow, J., Murphy, T., Meneus, L., Mihova, T., Mlenga, V., Morrow, J., Murphy, T., Nalyor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Plerre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,
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Homo sapiens clone RP11-240G10, WORKING DRAFT SEQUENCE, 27
unordered pieces.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-240G10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.9%; Score 23; DB 2; Length 145734; 83.9%; Pred. No. 1.5e+02; 1ve 0; Mismatches 5; Indels 0.
                                                                                                                         41083 41182: gap of 100 bp 41183 55282: contig of 14100 bp in length 55283 55382: gap of 100 bp 11365: contig of 55983 bp in length 111366 111465: gap of 100 bp 111466 145734: contig of 34269 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 others
                                                                                                       41082: contig of 41082 bp in length
                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RPCI-11 Human Male BAC"
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27856 c 27629 g 44978 t
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AC084188.2 GI:12229375
HTG: HTGS_PHASE1; HTGS_DRAFT.
Homo saptens.
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Best Local Similarity 83.9
Matches 26; Conservative
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ORIGIN
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VERSION
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AUTHORS
TITLE
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AC084188
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JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                              FEATURES
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Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, N., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Direct, and Zody, M.
                                                                                                                                                                                                                                                                                                                                Submitted (14-OCT-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 15, 2001 this sequence version replaced g1:10801416. All repeats were identifiabling RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Veb site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Contact: Project Information
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Center clone name: 240_G_10
Center clone name: 240_G_10
Center clone name: 240_G_10
Sequencing vector: Plasmid: n/a; 100% of reads
Chemistry: Dye-terminator Big Dye, 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 1412103 bases at least Q40
Consensus quality: 146385 bases at least Q30
Consensus quality: 148123 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 148935; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
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33534: contig of 22827 bp in length
33634: gap of 100 bp
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242 341: gap of 100 bp
342 3464: contig of 1323 bp in length
1665 1764: gap of 100 bp
1765 3932: contig of 2168 bp in length
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52274: contig of 4726 bp
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4032: gap of
5773: contig of
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7179 7278: gap of
7279 8531: conti-
8532 8631: gap of
8632 10607: conti-
10608 10707: gap of
10708 33534: conti-
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66288 66381; gap of 100 bp 66388 66389; gap of 100 bp 66388 7117; contig of 4730 bp in length 71218 77151; contig of 5934 bp in length 77152 77251; gap of 100 bp 77252 87532; contig of 10281 bp in length 87533 87623; gap of 100 bp 87633 87633; gap of 100 bp 94595 94694; gap of 100 bp 94595 94694; gap of 100 bp 10309 10308; contig of 8314 bp in length 10309 103108; gap of 100 bp 113635 113735; contig of 100 bp 113635 113735 contig of 100 bp 113735 1138598; contig of 100 bp 113735 113735 contig of 100 bp 1149706; gap of 100 bp 1149706; gap of 100 bp 1149706; contig of 100 bp 1149706; contig of 1730 bp in length 149706 149805; gap of 100 bp 116941.
820: gap of 100 bp 66287: contig of 4467 bp in length 387: gap of 100 bp 71117: contig of 4730 bp in length 217: gap of 100 bp 77151: contig of 5934 bp in length
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilae; Brachycera; Man.K.H.,

RS Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,

Rogers, Y., An.H., Baldwin, D., Banzon, J., Beson, K.Y., Busam, D.A.,

Carlson, J.W., Center, V., Champe, M., Davenport, L.B., Dietz, S.M.,

Carlson, J.W., Center, V., Doup, L.E., Doyle-C., Dresnek, D., Farfan, D.,

Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,

Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,

NeIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,

Pacleb, J., Paragas, V., Park, S., Patel, S., Pefeifer, B.,

Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,

Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,

Zaveri, J.S., Smith, H.O., Rublin, G.M. and Venter, J.C.

Upublished

Calliker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,

Bucenhoff, C., Champe, M., Chave, M., Ciesiolka, L.,

Doyle, C. M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,

Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,

Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,

Pholin, G. M.,

Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., and

Buhin, G. M.
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121

Berkeley, CA 94720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC008254 164982 bp DNA linear INV 17-FEB-2001
Drosophila melanogaster, chromosome 3R, region 85C-85C, BAC clone
BACR02632, complete sequence.
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44763 a 29429 c 29282 g 45460 t
                    Db 59894 AATATAACACAATATTACTTTTTTGTATGA 59924
/note="assembly_fragment"
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JOURNAL
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Db 12907 AACAAAGACAATATTAATTGTGTTATTTA 12877
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Eukaryota: Metaanogaster

Eukaryota: Arthropoda: Hexapoda: Insecta; Pterygota;

Reptera: Endopterygota: Diptera: Brachycera: Muscomorpha;

Ephydroides: Drosophilidae: Drosophila.

Esphydroides: Drosophilidae: Drosophila.

Esphydroides: Drosophilidae: Drosophila.

Esphydroides: Drosophilidae: Drosophila.

Edit.R.A. Evans.C.A. Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,

Rogers,Y., An.H., Baldwin,D., Banzon,J., Beson,K.Y., Busam,D.A.,

Rogers,Y., An.H., Baldwin,D., Banzon,J., Beson,K.Y., Busam,D.A.,

Rogers,Y., Morter,J., Chanpe,M., Davenport,L.B., Dietz,S.M.,

Ferriera,S., Frise,E. Galle,R.F., Garg,N.S., George,R.A.,

Ibegwam,C., Jalall,M., Kruse,D., Li,P., Mattel,B., Moshrefi,A.,

Mointosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,R.Y.,

Rogeleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,

Stapleton,M., Strong,R., Syirskas,R., Tector,C., Williams,S.M.,

Sequencing of Drosophila chromosome 3R, region 85C-85C

Celliker,S.E., Apbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,

Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,

Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Marda,P.,

Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,

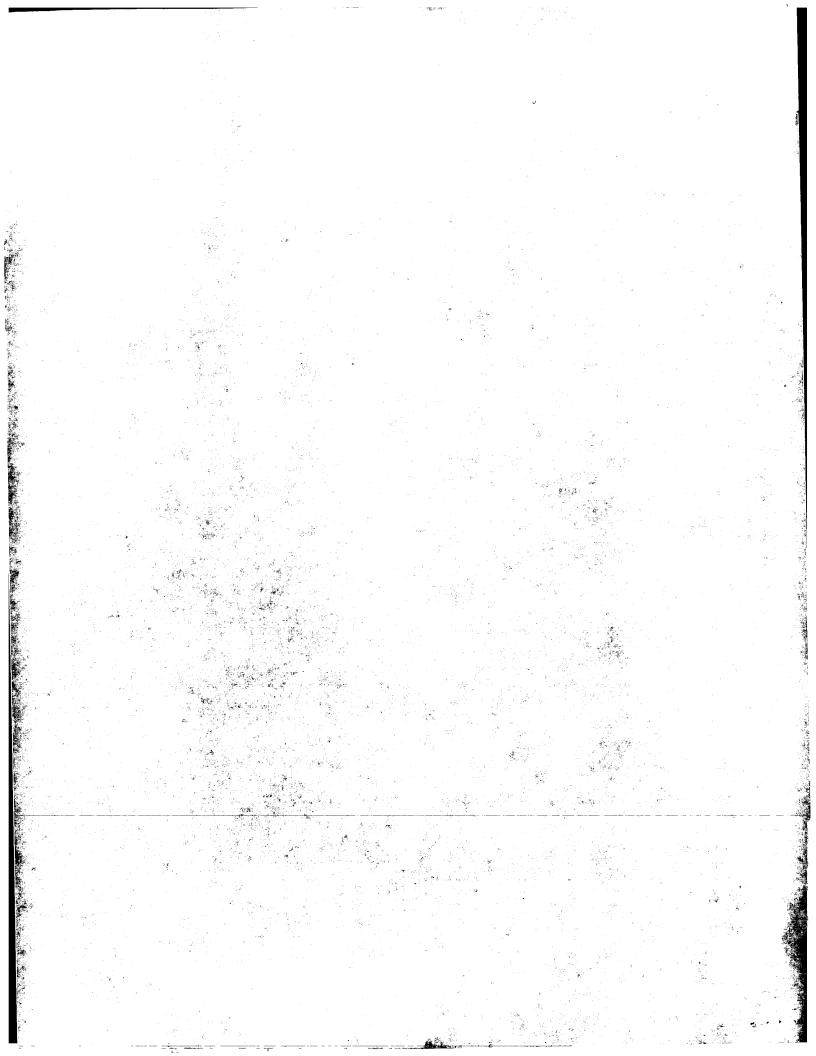
Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and

Rubin.G.M.
and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
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Submitted (09-AuG-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Feb 17, 2001 this sequence version replaced gi:5734650.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC009258
Drosophila melanogaster, chromosome 3R, region 85C-85C, BAC clone
                                                                                                                                                                                                                                      /clone="BACR02622 (D833)"
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
PBACE3.6)"
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                                                                                               1. .164982
/organism="Drosophila melanogaster"
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0; Mismatches
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                                                                                                                                              /strain="y; on bw sp"
/db_xref="taxon:7227"
/chromosome="3R"
/map="85C-85C"
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Drosophila melanogaster
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Best Local Similarity 83.9%;
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This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.orgware.

1. .176036
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                                                                                                                                                                           /organism="Drosophila melanogaster"
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/chromosome="3R"
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Human immune/haema Human immune/haema Tumour suppressor immune/haema

Human

Human immune syste

Genomic sequence #

Soybean 240017 reg Soybean 240017 reg Genomic sequence # Human immunoglobul Human eosinophil-m Human secreted pro Human secreted pro Drosophila melanog AmEPV genome fragm Arabidopsis thalia

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Drosophila melanogaster expressed polynucleotide SEQ ID NO 12908
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ABK53294
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AAI58011
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AAX00678
AAI59797
AAH51783
ABL32084
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ABK43029
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ABN18845
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AAQ12598
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11-JUL-2000; 2000US-0614150.
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 P-PSDB; ABB62039
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Venter JC,
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3. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1982.DAT:*

3. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1983.DAT:*

3. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1985.DAT:*

3. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1985.DAT:*

3. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1985.DAT:*

3. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1989.DAT:*

3. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1989.DAT:*

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3. /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*

3. /SIDS2/gcgdata/geneseq-embl/NA2000.DAT:*

3. /SIDS2/gcgdata/geneseq-geneseqn-embl/NA1990.DAT:*

4. /SIDS2/gcgdata/geneseq-geneseqn-embl/NA1990.DAT:*

4. /SIDS2/gcgdata/geneseq-geneseqn-embl/NA1990.DAT:*
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       5.1.3
Compugen Ltd.
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                                                                                                                                                                                                                                                          2185239 seqs, 1125999159 residues
       GenCore version
Copyright (c) 1993 - 2003
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                                                                  sw model
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Listing first 45 summaries
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AAX13684
AAX46482
AAK57011
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                                                               nucleic search, using
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seq length: 200000000
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Drosophila melanog Human ORFX polynuc Amplicon DNA compr Rat sequence diffe Pneumocystis carin Human colon cancer Pneumocystis carin P.carinii dihydrof Human polynucleoti

Human secreted pro Chromosome 13q31-q Human immune syste Orosophila melanog Orosophila melanog Human immune syste

Chemically pretrea

New isolated nucleic acid detection reagent for detecting 1000 or more

immune/haema

Human

Result No.

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Human ovarian anti Human polynucleoti

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infection
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                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
from Drosophila and for elucidating cell signalling and cell-cell
                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, theractions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           computer readable medium has been developed which has recorded on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
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                                                                                                                                                                                                                                                                                                                Length 28360;
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                                                 Claim 1; SEQ ID NO 12908; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                 5; Indels
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Pred. No. 81;
0; Mismatches
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97US-0046655.
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ilarity 83.3%;
Conservative
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nes 25; Conserv
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          genes
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 516 (actually 513 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid collapsementary to form the sequence listing is sequenced or nucleic acid-ollapsementary to (Ss). The nucleic acid may be a peptide nucleic acid-ollapsementary to (Ss). The nucleic acid may be a and/or single nucleotide polymorphisms and also to be used in an array for analyshing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific
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diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
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                                                                                                                                                                                                                                                                                                                    Score 21.4; DB 20;
Pred. No. 1.4e+02;
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ID AAS46482 standard; DNA; 12426
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2000DE-1019173.
2000DE-1032529.
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
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2000US-0225759.
2000US-0226279.
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2000US-0226868.
2000US-0227182.
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2000US-0228924.
2000US-0229287.
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2000US-0230437.
2000US-0230438.
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14-SEP-2000; 2000US-0232400
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14-SEP-2000; 2000US-0233065
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13-OCT-2000;
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diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and concegenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence ID 2 and ID 2 and ID 2 and ID 356 and ID 535, except for those whose partner sequence of the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:2071
                                                                                                                                                                                                                                                                          66.9%; Score 21.4; DB 22; Length 12426; 80.6%; Pred. No. 1.3e+02; Ative 0; Mismatches 6; Indels 0;
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ID AAK57011 standard; cDNA; 434 BP
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20000S-0189874
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2000US-0225447
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Matches 25; Conservative
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17-MAR-2000;
19-MAY-2000;
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20-JUN-2000;
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20-JUL-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) collynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent.

Conners and cancer metastases of haematopoietic acids especially cancer metastases of haematopoietic actived cells. AAK64703 concerns and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK87694 represent invention. AAK54942 to AAK87650 and AAAM82169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
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Best Local Similarity 91.7%; Pred. No. 2.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0;
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2000US-0249216.
2000US-0249217.
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2000US-0249244.
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2000US-0249299.
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P-PSDB; AAM84230.
08-NOV-2000;
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01-DEC-2000;
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24117.
         238 ATACAACACAAAATGAATTGTGTT 215
3 ATACAACACAATATTAATTGTGTT 26
                                                              AAK69305 standard; DNA; 440 BP.
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2000US-0227182.
2000US-0227009.
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2000US-0190076.
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05-SEP-2000; 2000US-0229509
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2000US-0231243
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28-JUN-2000;
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2000US-0233063.
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2000US-0236367.
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2000US-0236802.
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AAK$4951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic acitivity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) colynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent.

Cancers and cancer metastases of haematopoietic-derived cells. AAK64703 co AAK87694 represent invention. AAK54912 to AAK87950 and AAM82169 correspond to the present invention.
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cytostatic; gene therapy; vaccine; metastasis; ds,
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2000US-0250391.
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Matches 22, Conservative
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SCI INC HUMAN GENOME us-09-895-435-3.rng

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11-JUL-2000; 2000US-0217487.

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       AMESA951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cativity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (I) be expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) colynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent. (I) cancers and cancer metastases of haematopoietic acids diseases, especially cancers and cancer metastases of haematopoietic antigen genomic concers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK84950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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                                               Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                              Disclosure; SEQ ID NO 21167; 3071pp + Sequence Listing; English
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Rosen CA, Barash SC,
                        WPI; 2001-483426/52.
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the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic related diseases, especially cancers and cancer metastases of haematopoletic derived cells. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                              Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
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                                                                                                                                    Score 20.8; DB 22; Length 445;
Pred. No. 2.2e+02;
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AMES 4951 to AAK64702 encode the human immune/haematopoletic antigen (I) amino acid sequences given in AAM82170 to AAM91221. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased conversation by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) colynucleotides may be used to produce the secreted (I), by inscrting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, concers and cancer metastases of haematopoietic deilved cells. AAK64703 cancers and cancer metastases of haematopoietic deilved cells. AAK64703 cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54912 to AAK87950 and AAM82169 cerepresent invention. Cerepresent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 21308; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 445 BP; 98 A; 94 C; 112 G; 141 T; 0 other;
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Score 20.8; DB 22; Length 445; Pred. No. 2.2e+02; 0; Mismatches 2; Indels 0

y Match 65.0%; Local Similarity 91.7%; les 22; Conservative

Query Match Best Loca Matches

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          AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
cepression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
controlectides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
co AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK84950 and AAM82169
corrected to the present invention. AAK54942 to AAK84950 and AAM82169
                                                                                                                                                                                                                                          Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 21311; 3071pp + Sequence Listing; English
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ID AAK69304 standard; DNA; 445 BP.

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AC AAK69304 standard; DNA; 445 BP.

XX
DT 06-NOV-2001 (first entry)

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KW
Human; immune/haematopoietic antign

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KW
Cytostatic; gene therapy; vaccine

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NOCO157182-A2.

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PD 09-AUG-2001.

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PF 17-JAN-2001; 2001WO-US01354.
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                                          2000US-0251856.
2000US-0251868.
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2000US-0251989.
2000US-0251990.
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                 2000US-0256719
2000US-0251479
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  2000US-0251988
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05-DEC-2000;
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Disclosure; SEQ ID NO 24116; 3071pp + Sequence Listing; English.

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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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000US-0244617.
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17-NOV-2000;
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AAK AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM83170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)

proteins and polynuclectides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)

concluded any be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
concers and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
concers and cancer human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK54950 and AAM82169
represent sequences used in the exemplification of the present invention.
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nes 22; Conservat
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17 NOV-2000; 2000GS-0249264.
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Rosen CA, Barash SC, Ruben SM (HUMA-) HUMAN GENOME SCI INC

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 24118; 3071pp + Sequence Listing; English.

AMES 4951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cactivity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased carples on by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) colynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, (C) protein. (I) proteins and polynucleotides may be used to prevent, (C) adagnose and freat imune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic concers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK87691 and AAM82169 represent sequences used in the exemplification of the present invention.

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cytostatic; gene therapy; vaccine; metastasis; ds.
                                                    Gaps
                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24119
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         Sequence 445 BP; 141 A; 112 C; 94 G; 98 T; 0 other;
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28-JUN-2000;
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AAK69307/C
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39670
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11-JUL-2000; 2000US-0217487
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2000US-0224518.
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2000US-0227182
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02-MAR-2000;
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14-AUG-2000;
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14-AUG-2000;
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              AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cativity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention. (I) expression by rectifying mutations or deletions in a patient's genome cample, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) colynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent. (C) the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent. (C) adagnose and treat immune/haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic antigen genomic concers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK84950 and AAM82169 crepresent invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                                                                                                        2000US-0249299
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2000US-0249300
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectivity of (I) by expressing inactive proteins or to that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) colynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein: (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially connects and cancer metastases of haematopoietic derived cells. AAK64703 concerns and cancer metastases of haematopoietic antigen genomic concerns and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK87694 represent invention. AAK54942 to AAK87650 and AAM82169 crepresent invention.
                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 39670; 3071pp + Sequence Listing; English.
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2000US-0186350.
2000US-0199074.
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                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
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11-DEC-2000; 2000US-0254097.
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07-JUN-2000;
30-JUN-2000;
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14-SEP-2000;
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13-OCT-2000;
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20000US - 0241221 2000US - 0241785 2000US - 0241786 2000US - 0241786 2000US - 0241808 2000US - 0241808 2000US - 024647 2000US - 0246476 2000US - 0246476 2000US - 0246476 2000US - 0246523 2000US - 0246526 2000US - 0246511 2000US - 024920 2000US - 0249211 2000US - 0249211 2000US - 0249214 2000US - 0249216 2000US - 0249214 2000US-0249245. 2000US-0249264. 2000US-0249265. 2000US-0249265. 2000US-0249299. 2000US-0249300. 2000US-0250160. 2000US-0250391. 2000US-0251030. 2000US-0251988. 2000US-0256719. 2000US-0251479. 2000US-0251856. 2000US-0251868. 2000US-0251869. 2000US-0251989. 2000US-0251990. 2000US-0254097. 2001US-0259678 01-DEC-2000; 05-DEC-2000; 05-DEC-2000; 06-DEC-2000; 06-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 2 11-DEC-2000; 2 05-JAN-2001; 2 20-0CT-2000;
20-0C

(HUMA-) HUMAN GENOME SCI INC

Ruben Barash SC, Rosen CA,

WPI; 2001-483426/52

human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and Nucleic acids encoding useful for preventing, metastasis -

Disclosure; SEQ ID NO 39674; 3071pp + Sequence Listing; English.

AAKS4951 to AAK64702 encode the human immune/haematopoletic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and

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treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) by lonucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a hostociec the secreted (1), by inserting protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of hematopoietic antigen genomic sequences from the present innumer/haematopoietic antigen genomic
                                                                                                                                                                                                                                                                                                                                                                 represent sequences used in the exemplification of the present invention.
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Sequence 445 BP; 98 A; 94 C; 112 G; 141 T; 0 other;

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0
                             Gaps
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0
 Score 20.8; DB 22; Length 445; Pred. No. 2.2e+02;
                            Indels
                          0; Mismatches
                                                                 211 ATACAACACAAAATGAATTGTGTT 234
                                                   3 ATACAACACAATATTAATTGTGTT 26
65.08;
91.78;
           Local Similarity 91.7 nes 22; Conservative
   Query Match
                            Matches
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Tumour suppressor gene derived chemically modified sequence #198 BP AAS46476 standard; DNA; 13377 (first entry) 18-DEC-2001 AAS46476; RESULT 15 AAS46476

Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP; cancer; tumour; CpG dinuc cytosine methylation; ds.

WO200168912-A2 Homo sapiens.

20-SEP-2001

15-MAR-2001; 2001WO-EP02955.

06-APR-2000; 2 07-APR-2000; 2 30-JUN-2000; 2 15-MAR-2000;

2000DE-1019058. 2000DE-1019173. 2000DE-1032529. 2000DE-1043826. 01-SEP-2000;

(EPIG-) EPIGENOMICS AG.

Berlin Olek A, Piepenbrock C,

WPI; 2001-602752/68.

Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g. cancer

Claim 1; SEQ ID No 198; 27pp; English.

The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (SS) and sequences complementary to (SS). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may

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form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analyysing diseases associated with Cpc dinucleotides e.g. cancers and tumnours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis of and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the concomplementary sequences derived from tumour suppressor genes and concogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and IDI, ID 536 and ID 535, except for those whose partner sequence is missing).

Note: The sequence data for this patent did not form part
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Pred. No. 2.1e+02;
0; Mismatches 7; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5498 TTATATAAAAGAATATTAATTACGTGGTATTA 5529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
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completed: February 13, 2003, 01:45:42 300 secs Search co Appli Appli

Sequence 11, Ap Sequence 13, Ap Sequence 26, Ap Sequence 27, Ap Sequence 37, Ap Sequence 30, Ap Sequence 37, Ap Sequence 4, App Sequence 4, App Sequence 4, App Sequence 67, Ap Sequence 87, App Sequence 87, App

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Patent No. 5164490

PAPLICANT: SAWIT, DANIEL V.:EDMAN, JEFFREY:EDMAN, URSULA
TITLE OF INVENTION: PNEUMOCYSTIS CARINII DIHYDROFOLATE
TUMBER GENE AND METHODS FOR ITS USE
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/437,511
FILING DATE: 15-NOV-1989
US-07-966-187-11

US-07-966-187-13

US-09-561-825-1

US-09-561-825-26

US-09-561-825-29

US-09-561-825-29

US-09-561-825-28

US-09-581-148C-30

US-09-026-039-3

US-08-036-165A-105

US-08-936-165A-105

US-08-08-036-105

US-08-050-032-036-105

US-08-050-032-036-105

US-08-08-036-105

US-08-08-036-105

US-08-680-726A-85

US-08-680-726A-85
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77.4%; Pred. No. 48;
iive 0; Mismatches
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US-08-770-941-13

| Sequence 13. Application US/08770941
| Patent NO. 6025133
| GENERAL INFORMATION:
| APPLICANT: Stull, Paul D. |
| APPLICANT: Myers, Kristi K. |
| APPLICANT: Becker, Michael M. |
| TITLE OF INVENTION: AMPLIFICATION ITALE OF INVENTION: AMPLIFICATION INVERSES: 23 |
| CORRESPONDENCE ADDRESS: 3 |
| ADDRESSEE: Lyon & Lyon |
| STREET: G13 West Fifth Street |
| STREET: G114 4700 |
| CITY: Los Angeles |
| CONTRESSES |
| CONTRESSES |
| STREET: CALLIGATION |
| STREET: CALLIGATION |
| STREET: CALLIGATION |
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIBLE
SOPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/770,941
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ZIP: 90071-2066
    SEQ ID NO:2:
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Sequence 13, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 11, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 29, Appl
Sequence 2, Appl
Sequence 2, Appli
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-134-001C-2702
US-09-134-17
US-09-54-185-17
US-08-687-080-86
US-08-964-320-1
US-08-94-320-1
US-08-37-6538-1
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US-08-984-320-2
US-08-487-087A-2
US-08-397-653B-2
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US-08-591-629-7
US-09-426-290-1
US-08-485-568A-3
US-08-357-698-5
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US-08-308-872B-5
US-09-173-300-50
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                 - nucleic search, using sw model
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Maximum DB
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GENERAL INFORMATION:
APPLICANT: FULUIChI, Yasuhiro
APPLICANT: Hoshino, Tatsuo
APPLICANT: Kimura, Hitoshi
APPLICANT: Kimura, Hitoshi
APPLICANT: Kimura, Hitoshi
APPLICANT: Nagahashi, Yoshie
ITILE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
FILE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
CURRENT APPLICATION NUMBER: US/09/594,185
CURRENT APPLICATION NUMBER: 08/935,263
PRIOR FILING DATE: 1997-09-22
PRIOR FILING DATE: 1997-09-27
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PALCHIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (302)..(358)
OTHER INFORMATION: Partial sequence of ORF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19.2;
Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: Complement((1)..(58))
CTHER INFORMATION: Partial sequnce of ORF1.
US-08-935-263-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 TAATIGAACAATATTTTATTTGTGTGTTATTA 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (244)...(283)
OTHER INFORMATION: BOX2 - inverted repeat
CURRENT APPLICATION NUMBER: US/08/935,263A CURRENT FILING DATE: 1997-09-22 EARLIER APPLICATION NUMBER: EP 96115540.5 EARLIER FILING DATE: 1996-09-27 NUMBER OF SEQ ID NOS: 23 SOFTWARE: Patentin Ver: 2.1 SEQ ID NO 17

    inverted repeat

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                                                                                                                                                                                                                                                                                                                                                                                                                   -10_signal Complement((235)..(240))
                                                                                                                                                                                                                                      NAME/KEY: RBS
LOCATION: Complement((67)..(76))
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LOCATION: (125)..(164)
OTHER INFORMATION: BOX1
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                                                                                                                                                                                                                                                                                              NAME/KEY: -35_signal LOCATION: (210)..(215)
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: -10_signal LOCATION: (234)..(239)
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LOCATION: (289)..(293)
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Best Local Similarity
Matches 24; Conserva
                                                                                                                                                                                             ORGANISM: Kurthia sp
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US-09-594-185-17
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                                                                                                                                                                          TYPE: DNA
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US-09-134-001C-2702/C
Sequence 2702, Application US/09134001C
Federal Care 2702, Application US/09134001C
Federal Care: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: BFIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DETIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
FRIOR APPLICATION NUMBER: US 60/064,964
FRIOR FILING DATE: 1997-11-08
FRIOR FILING DATE: 1997-11-08
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2702
LENGTH: 342
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APPLICANT: Furnichi, Yasuhiro
APPLICANT: Furnichi, Tatsuo
APPLICANT: Kimura, Hitoshi
APPLICANT: Kiyasu, Tatsuya
APPLICANT: Niyasa, Tatsuya
TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19.2; DE Pred. No. 85; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-2702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-935-263-17; Sequence 17, Application US/08935263A; Patent No. 6117669
                                                                                                                                                                                   212/284
    FILING DATE: Herewith CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 212/2
TELECOMMUNICATION INFORMATION:
TELEFONE: (213) 489-1600
TELEFAX: (7-3510
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDENBESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: Biotin Genes
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Best Local Similarity 75.03
Matches 24; Conservative
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Best Local Similarity
Matches 24; Conserv
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US-08-770-941-13
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LENGTH: 266 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDREL ISETTE TO DAVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 95616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-984-320-1/c
                                                                                                                                                                                                                                                                                                                                                    us-080-687-080-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human RAD50 Gene and Methods of Use Thereof
175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOCATION: (402)...(435)
NAME/KEY: misc feature
LOCATION: (302)...(358)
OTHER INFORMATION: Partial sequence of ORF2.
NAME/KEY: misc feature
LOCATION: (125)...(164)
OTHER INFORMATION: BOXI - inverted repeat
NAME/KEY: misc feature
LOCATION: (244)...(283)
OTHER INFORMATION: BOXZ - inverted repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 86, Application US/08687080
Patent No. 5965427
GENERAL INFORMATION:
APPLICANT GREGOTY DOLGANOV
TITLE OF INVENTION: Human RAD50 Gene and Met)
NUMBER OF SEQUENCES: 175
CORRESPONDENCE DORESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STRATE: CA
COUNTY: USA
COUNTY: USA
COMPUTER READBLE FORM:
MEDIUM READBLE FORM:
MEDIUM PER FEADBLE FORM:
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DEFORM:
COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Best Local Similarity 75.0%; Pred. No. 80;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KBY: misc_feature

! LOCATION: Complement((1)..(58))

OTHER INFORMATION: Partial sequnce of ORFI.

US-09-594-185-17
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APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        LOCATION: (234)...(239)
NAME/KEY: -10_signal
LOCATION: Complement((235)..(240))
                                                                                                                                                 Complement((67)..(76))
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REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               -35_signal
(210)..(215)
-10_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                      . (293)
                                     ORGANISM: Kurthia sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (289).
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                                                                                                                   NAME/KEY:
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Gaps
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APPLICANT: McBride, Kevin E.
APPLICANT: McBride, Mcwin E.
APPLICANT: Stalker, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calque, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                          ;
0
TOPOLGGY: linear MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 3' END OF INTRON 13 OF RAD50 GENOMIC
                                                                                                                                                                                                                              Length 266;
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                               Query Match 58.8%; Score 18.8; DB 2; Best Local Similarity 76.7%; Pred. No. 1.1e+02; Matches 23; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087
FILING DATE: 07-UNH-95
APPLICATION NUMBER: US/08/487,087
FILING DATE: 99-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/195
FILING DATE: 17-UUL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/195
FILING DATE: 19-UUL-89
ATTONNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
                                                                                                                                                                                                                                                                                                                                        160 AAAAGAACACAATGTCACTTCTGTGGTATT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Carl J. Schwedler
REGISTRATION NUMBER: 34,719
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
                                                                                                                                                                                                                                                                                                          2 AATACAACAATATTAATTGTGTGTTTT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,320
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08984320 Patent No. 6222097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1310
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
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linear
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ZIP: 95616
                                                                                                                                                               Davis
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; LENGTH: 564
US-08-397-653B-1/C
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                                                        0;
                                                          Gaps
                                                                                                                                                           RESULT 8
US-08487-087A-1/C
US-08487087A
; Sequence 1, Application US/08487087A
; Patent No. 6268546
; GENERAL INFORMATION:
APPLICANT: McEride, Kevin E.
APPLICANT: Stalker, David M.
; TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCES: 6
; CORRESPONDENCES: 7
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                              Query Match 58.8%; Score 18.8; DB 4; Length 564; Best Local Similarity 76.7%; Pred. No. 1.1e+02; Matches 23; Conservative 0; Mismatches 7; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Diskette, 3.50 inch, 1.4 MB
                                                                                                                                                                                                                                                                                                                                                                                                   2 AATACAACACAATATTAATTGTGTŢGTATT 31
                                                                                                                  423 AAGGCAACACTTTATTAATTTTGTTTTTT 394
                                                                                       2 AATACAACACAATATTAATTGTGTTGTATT 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
US-08-487-087A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 76.7
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                             ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                               STREET: 1920
CITY: Davis
                                                                                                                                                                                                                                                                                                                                         STATE: C.
        US-08-984-320-1
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"RESULT 9

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5175095-1/c
; Patent No.5175095
APLICANT: Martineau, Belinda M.; Houck, Catherine.M. APPLICANT: Martineau, Belinda M.; Houck, Catherine.M. TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS; NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/554,195
FILING DATE: 17-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18.8; DB 4;
Pred. No. 1.1e+02;
                                                                                 COTTON MODIFICATION USING OVARY-TISSUE TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                             ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh 7.0
SOFTMARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,653B
FILING DATE: 28 FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.16
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 AAGGCAACACTITATTAATTTTGTTTTT 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
Sequence 1, Application US/08397653B Patent No. 6329570 GENERAL INFORMATION:
                                                           APPLICANT: Martineau, Belinda
TITLE OF INVENTION: COTTON MODIT
TITLE OF INVENTION: COVARY-TISSUI
TITLE OF INVENTION: PACTORS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (916) 753-6313
TELEPRAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.8%;
76.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 76.73
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 76.73
Matches 23; Conservative
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Gaps
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APPLICANT: Stalker, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18.8; DB 4;
Pred. No. 1.1e+02;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,320
                                                  TITLE OF INVENTION PESTICIDAL PROCESSING TITLE OF INVENTION PESTICIDAL PROCESSING TITLE REFERENCE: MA703C2 CURRENT APPLICATION NUMBER: US/09/378,088A CURRENT FILING DATE: 1999-08-20 PRIOR PAPLICATION NUMBER: US 08/633,993 PRIOR FILING DATE: 1996-04-19 PRIOR FILING DATE: 1997-04-18 PRIOR FILING DATE: 1997-04-18 NUMBER OF SEQ ID NOS: 130 SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087
FILING DATE: 07-UN-95
APPLICATION NUMBER: US/08/487,087
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/195
FILING DATE: 17-UL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/07/382,518
FILING DATE: 19-JUL-89
ATTONEY, AGENT INFORMATION:
NAME: PORTER SCHOOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      724 AATACCAAAAATATTTATTTTTGGTATT 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AATACAACACAATATTAATTGTGTGTATT 31
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REFERENCE/DOCKET NUMBER: GGNE 91-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/08984320; Patent No. 6222097; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-378-088A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34,719
                Finstad Lee, Stacy
Burmeister, Paula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Calgene, Inc. STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 58.8%;
Best Local Similarity 76.7%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Donna E. Scherer
REGISTRATION NUMBER: 34
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-08-984-320-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                             SEQ ID NO 39
LENGTH: 2132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: C
COUNTRY:
                                   APPLICANT:
APPLICANT:
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Pred. No. 1.1e+02;
0; Mismatches 7; Indels 0
                                                                                                                                                                          APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnebf, Mark
APPLICANT: Pollard, Michael R.
APPLICANT: Pollard, Michael R.
APPLICANT: Pollard, Gorige E.
TITLE OF INVENTION: Pesticidal Toxins
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: LACION W. 41st Street, Suite A-1
STATE: The Compatible
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING PSSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING NSTEM: DATA:
APPLICATION NUMBER: US/08/844,188
FILING DATE:
APPLICATION NUMBER: US/08/844,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/633,993
FILING DATE: 19-APR-1996
CLASSIFICATION NUMBER: US 08/633,993
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-703C1
TELEPHONE: 352-375-8100
TELEPRX: 352-375-8100
TELEPRX: 352-375-8100
TELEPRX: 352-375-8100
TELEPRX: MANAMEDIAL SALVEN SEQ ID NO: 39:
423 AAGGCAACACTTTATTAATTTTGTTTTTT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AATACAACACAATATTAATTGTGTTGTATT 31
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Patent No. 6372480
GENERAL INFORMATION:
APPLICANT: Narva, Kenneth E.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Knuth, Mark
APPLICANT: Cardineau, Guy A.
APPLICANT: Schwab, George E.
APPLICANT: Schwab, George E.
                                                                                                           Sequence 39, Application US/08844188 Patent No. 6127180 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.8%;
Best Local Similarity 76.7%;
Matches 23; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2132 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-09-378-088A-39/c
                                                                                        US-08-844-188-39/C
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Sequence 2. Application US/08487087A
Sequence 2. Application
Series Information:
APPLICANT: MoBride, Kevin E.
APPLICANT: Stalker, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                               Score 18.8; BB 4; Length 3528;
Pred. No. 1e+02;
0; Mismatches 7; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: MICROSOft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087A
FILING DATE: 07-JUN-95
CLASSIFICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
RELING DATE: 19-JUL-90
PRIOR APPLICATION DATA:
RELING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scheret
RECISTRATION NUMBER: 34,719
NAME: CALI J. SCHWEGLET
RECISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                             3241 AAGGCAACACTTTATTAATTTGTTTTTT 3212
                                                                                                                                                                                                                                                                                                                    2 AATACAACACAATATTAATTGTGTTGTATT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    Query Match 58.8%;
Best Local Similarity 76.7%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: genomic DNA
                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-984-320-2
                                             LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-08-487-087A-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                               COTTON MODIFICATION USING OVARY-TISSUE TRANSCRIPTIONAL FACTORS
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                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: February 13, 2003, 04:52:39 Job time: 71\ \mathrm{secs}
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                      3241 AAGGCAACATTTATTAATTTTGTTTTTT 3212
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2 AATACAACACAATATTAATTGTGTGTATT 31
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28-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGNE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: MICROSOFT WORD S. 1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,65
FILING DATE: 28-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: ELizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: GGNE 11
TELECOMMUNICATION INFORMATION:
                                                                                                                %3-08-397-653B-2/c

Sequence 2, Application US/08397653B

Patent No. 6328570

GENERAL INFORMATION:

APPLICANT: Martineau, Belinda
                                                                                                                                                                                             Martineau, Belinda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.8%;
76.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                             ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 4383 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23; Conservative
                                                                                                                                                                                                             TITLE OF INVENTION: COTTITLE OF INVENTION: COVAR TITLE OF INVENTION: PACTIONERS OF SOURCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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STATE:
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Sequence 1276. Appli Sequence 8, Appli Sequence 19, Appli Sequence 19, Appl Sequence 114, Appl Sequence 117, Appl Sequence 117, Appl Sequence 118, Appl Sequence 118, Appl Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 31229, Appli Sequence 102, Appli Sequence 102, Appli Sequence 106, Appli Sequence 1075, Appli

US-10-138-221-8 US-10-138-221-8 US-10-138-221-8 US-10-138-221-8 US-09-070-927A-19 US-09-070-927A-19 US-09-164-910-19 US-09-764-904-137 US-09-764-904-137 US-09-764-904-137 US-09-764-904-137 US-09-777-347-2 US-09-781-558-3 US-09-844-761-4375 US-09-844-761-4375 US-09-98-842A-3970 US-09-98-842A-3970 US-09-98-842A-3970 US-09-98-842A-3970 US-09-98-842A-3970 US-09-98-842A-3970 US-09-98-842A-3970

US-09-764-869-1276

US-09-887-576-196 US-09-960-352-222 US-09-960-352-2087 US-09-880-107-138 US-09-880-107-1875

100000

ALIGNMENTS

40,302

Hoover

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TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: H Vecttra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Paxt
CURRENT APPLICATION DATE: US.09/070,927A
FILING DATE: 04-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                         Sequence 747, Application US/09070927A Patent No. US20020120116A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 747:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kenley K. Hoove
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
 360
374
26225
4565
4565
4810
25580
302250
                                                                                                                                         3528
74586
74586
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2000
3029
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 US-09-070-927A-747/C
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Sequence 3, Appli
Sequence 770, App
Sequence 11904, A
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Sequence 4932, Ap
Sequence 4407, Ap
Sequence 1916, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 739, App
Sequence 217, App
Sequence 217, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 596, App
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Sequence 3174, Ap
Sequence 6, Appli
                                                           February 13, 2003, 01:41:21; Search time 37 Seconds (without alignments) 440.496 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                               / CGGG_E_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
/ CGGG_E_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
/ CGGG_E_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/ CGGG_E_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/ CGGG_E_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/ CGGG_E_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
/ CGGG_E_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
/ CGGG_E_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ CGGG_E_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ CGGG_E_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ CGGG_E_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ CGGG_E_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seg:*
 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-960-352-3174
US-09-835-232-6
                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                  424239 seqs, 254661826 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                      Published_Applications_NA:*
                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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1876
18501
335913
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; SEQ ID NO 4407
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4407
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nilarity 78.1%;
Conservative (
                                                                                                                                                                            Ouery Match 65.0%;
Best Local Similarity 78.1%;
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-09-764-847-1916/c
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US-09-754-853A-2
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Sequence 4407, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: HAIPER, Joel

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

TILE OF INVENTION: SAME, AND METHODS OF DIANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIPIAGO - 3

CURRENT FILING DATE: 2001-08-24

CURRENT FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2000-08-24
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Sequence 4932, Application US/09938842A

Sequence 4932, Application US/09938842A

Sequence 4932, Application US/09938842A

Sequence 4932, Application US/09938842A

SERIEMATION: Kreps, Joel

APPLICANT: Harper, Jeff

APPLICANT: Rreps, Joel

APPLICANT: SANG, Xun

APPLICANT: SANG, Yun

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIPI300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                                                                                                                 Length 1112;
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Pred. No. 65;
0; Mismatches
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80.6%; Pred. No. 64
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SEQUENCE DESCRIPTION: SEQ ID NO: 747:
US-09-070-927A-747
                                                                                                                                                                                                                                                                                                                                                                                       2 AAIACAACACAATAITAAITGIGITGIATIA 32
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                            LENGTH: 1112 base pairs
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4932
                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                 Query Match 66.9%;
Best Local Similarity 80.6%;
Matches 25; Conservative
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Best Local Similarity 80.65
Matches 25; Conservative
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US-09-938-842A-4407
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Sequence 2, Application US/09754853A
; Sequence 2, Application US/0905491A1
; GENERAL INFORMATION:
    APPLICATION PARTICION:
    APPLICANT: Hauge, Brian M.
; APPLICANT: Parsons, Jereny D.
; APPLICANT: Parsons, Jereny D.
; APPLICANT: Wang, Ming Li,
    TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
    TITLE OF INVENTION: Soybean Cyst Nematode Resistance
    FILE REFERENCE: 38-10(15810)B
; CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
; PRIOR PLICATION NUMBER: US 60/174,880
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 1119
; SEQ ID NOS: 1119
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       Length 1876;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEC ID NOS: 2003
SOFTWARE: PATENTIN VOS: 2.0
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Score 20.8; DB 9;
Pred. No. 1e+02;
0; Mismatches 7;
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Pred. No. 97;
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                                                                                                                             1 TAATACAACACAATATTAATTGTGTTGTATTA 32
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LOCATION: (9022)
OTHER INFORMATION: n equals a,t,9, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (9023)
; OTHER INFORMATION: n equals a,t,9, or
US-09-764-847-1916
                                                                                                                                                                                                                                                               Sequence 1916, Application US/09764847; Patent No. US20020132767A1; GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21/102991C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEO ID NOS: 15112
SEQ ID NO 11904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: Bos taurus
COTHER INFORMATION: Clone ID: 51-LIB3057-016-Q1-K1-E4
US-09-960-352-11904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCORMATION: USLOUZULI9462A1

APPLICANT: Mendrick, Donna
APPLICANT: Mendrick, Donna
APPLICANT: Johnson, Kary
APPLICANT: Johnson, Kary
APPLICANT: Castle, Arthur
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-us
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2000-11-02
PRIOR PELING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/290,45
PRIOR PELING DATE: 2001-05-15
PRIOR PELING DATE: 2001-05-15
PRIOR PELING DATE: 2001-05-15
PRIOR PELING DATE: 2001-05-16
PRIOR PELING DATE: 2001-05-17
PRIOR PELING DATE: 2001-05-19
PRIOR PELING DATE: 2001-05-19
PRIOR PELING DATE: 2001-06-19
PRIOR PELING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR PELING DATE: 2001-06-19
PRIOR PELING DATE: 2001-06-19
PRIOR PELING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SEQ ID NO 739
LENGTH: 562
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.1%; Score 20.2; DB 10;
88.0%; Pred. No. 1.6e+02;
Live 0; Mismatches 3;
                               RESULT 8
US-09-960-352-11904/c
; Sequence 11904, Application US/09960352
; Patent No. US20020137139A1
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; Sequence 739, Application US/09917800A
; Patent No. US20020119462A1
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Best Local Similarity
"a+rhes 22; Conserva
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Publication No. US20030005491A1

GENERAL INFORMATION:

APPLICANT: Hauge, Brian M.

APPLICANT: Parnell, Laurence D.

APPLICANT: Parnell, Laurence D.

APPLICANT: Parnell, Laurence D.

APPLICANT: Wang, Ming Li,

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

TITLE OF INVENTION: Soybean Cyst Nematode Resistance

TITLE OF INVENTION: Soybean Cyst Nematode Resistance

CURRENT APPLICATION NUMBER: US/09/754,853A

CURRENT FILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: US 60/174,880

NUMBER OF SEQ ID NOS: 1119

SEQ ID NOS: 1119
; LOCATION: (45163)..(4514),(45450)..(45509),(46941)..(48763),(48975)..(49573)
; OTHER INFORMATION: CLONE ID: 240017_region_G3
US-09-754-853A-2
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Patent No. US20020094953A1
GEMERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1198
SOFTWARE: PatentIn Ver. 2.0
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80.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 6;
                                                                                                                                                                                                                               Db 311066 TAATACAAAATGAGATTAATGTTATGTATA 311097
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; COCATION: (46798)..(48763),(48975)..(49573)
; OTHER INFORMATION: CLONE ID: 240017_region_G3
US-09-754-863A-3
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                                                                                               Query Match 65.0%; Score 20.8; Dest Local Similarity 78.1%; Pred. No. 88; Matches 25; Conservative 0; Mismatches
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Best Local Similarity 78.1%; Pred. No. 88;
Matches 25; Conservative 0; Mismatches
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Best Local Similarity 80.09
Matches 24; Conservative
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CORGANISM: HOMO Sapiens
US-09-764-860-770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Glycine max
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LENGTH: 504
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APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
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Best Local Simi
Matches 24;
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LENGTH: 2776
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                           ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AI102871
US-09-917-800A-739
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Best Local Similarity 77.4%; Pred. No. 2.2e+02;
Matches 24; Conservative 0; Mismatches 7; Indels
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                                                                                                                                                                        451 TAGGTCAAAACAATATTAATTGTGCCTTATT 421
                                                                                                                                           1 TAATACAACACAATATTAATTGTGTTGTATT 31
                                                                                                                                                                                                                                                        sequence 217, Application US/10098841 publication No. US20020197679A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: mis6_feature

! CCATION: (1)...(1936)

OTHER INFORMATION: n = a,t,c or g

US-10-098-841-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang, Jie
Qian, Xiaohong B.
                                                                                                                                                                                                                                                                                                           APPLICANT: Tang, X. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Xhou, Ping
APPLICANT: May Yunging
APPLICANT: May Yunging
APPLICANT: Rep, 7ian-Rui
APPLICANT: Rep, 7ian-Rui
APPLICANT: Rep, Reiyan
APPLICANT: Ren, Rui-hong
APPLICANT: Wang, Duntui
APPLICANT: Weng, Duntui
APPLICANT: Weng, Zhiwei
APPLICANT: Wehrman, Tom
     ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (81)..(752)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (81)
                                                                                                                                                                                                                                  RESULT 10
US-10-098-841-217
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APPLICANT:
APPLICANT:
APPLICANT:
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Gaps
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ilarity 77.4%; Pred. No. 2.1e+02;
Conservative 0; Mismatches 7;
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CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-19
PRIOR PILING DATE: 1998-03-19
PRIOR FILING DATE: 1997-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1997-03-24
PRIOR PLILING DATE: 1997-03-21
PRIOR PLLING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR PPLICATION NUMBER: US 60/048,188
PRIOR PPLICATION NUMBER: US 60/048,188
PRIOR APPLICATION NUMBER: US 60/048,188
PRIOR APPLICATION NUMBER: US 60/048,187
PRIOR PLILING DATE: 1997-05-30
PRIOR PLILING DATE: 1997-05-30
PRIOR PLILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,187
PRIOR PLILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,187
PRIOR PLILING DATE: 1997-05-30
PRIOR PLILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,186
PRIOR PLILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,186
PRIOR PLILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,131
PRIOR PRILING DATE: 1997-05-30
PRIOR PILING DATE: 1997-05-30
PRIOR PILING DATE: 1997-05-30
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PRIOR PRILING DATE: 1997-06-30
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-984-245-78
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; Sequence 78, Application US/09984245 ; Patent No. US20020165374A1

RESULT 11 US-09-984-245-78

0;

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APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOO1160
CURRENT APPLICATION NUMBER: US/09/801,876B
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 148567;
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APPLICANT: Allen, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Nelih
APPLICANT: Hoffman, Nelih
APPLICANT: Huckan, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Thallana
FILE REFERENCE: 2029 (PARA-018PRV)
CURRENT APPLICATION NUMBER: US/09/770,791
CURRENT FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-01-27
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SCOTTWARE FastSEQ for Windows Version 4.0
SEQ ID NO 596
LENGTH: 357
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US-09-770-791-596
Sequence 596, Application US/09770791
Patent No. US20020062014A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
                                                                                                                                                                                                                                                                                                                            , LUCATION: (1)...(148567); OTHER INFORMATION: n = A,T,C or GUS-09-801-8768-3
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Haas, William David
Garcia, Carlos A.
Kricker, Maja
Slader, Ted
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Rameaka, Joshua G.
Page, Amy Abraham V.
Ledford, Brooke L.
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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; ORGANISM: Arabidopsis thaliana
US-09-770-791-596
                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (1)...(148567
                                                                                                                                                                                                                                                                  ORGANISM: Human
                                                                                                                                                                                                 SEQ ID NO 3
LENGTH: 148567
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                                       Sequence 1, Application US/09754853A

Publication No. US20030005491A1

GENERAL INFORMATION:

APPLICANT: Hauge, Brian M.

APPLICANT: Parnell, Laurence D.

APPLICANT: Parnell, Laurence D.

APPLICANT: Wang, Ming Li

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-10(15810)B

CURRENT APPLICATION NUMBER: US/09/754,853A

CURRENT FILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: US 60/174,880

NUMBER OF SEQ ID NOS: 1119

SEQ ID NOS: 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-10-254-869-3/C
Sequence 3, Application US/10254869;
Publication No. US20030027307a1
GENERAL INFORMATION:
APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOJIGODIV
CURRENT APPLICATION NUMBER: US/10/254,869
CURRENT FILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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77.4%; Pred. No. 1.9e+02;
tive 0; Mismatches 7; Indels
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61.9%; Score 19.8; DB 9;
Best Local Similarity 77.4%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 7;
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; OTHER INFORMATION: Clone ID: 515002_region_G2
US-09-754-853A-1
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Patent No. US20020127683A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : NAME/KEY: misc_feature

: LCCATION: (1)...(148567)

: OTHER INFORMATION: n = A,T,C or G

US-10-254-869-3
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Best Local Similarity 77.44
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Glycine max
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 127197
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US-09-801-876B-3/C
  RESULT 12
US-09-754-853A-1
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Search completed: February 13, 2003, 04:56:51 Job time: 241 secs

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AL272948.1 GI:7995193
AL272948.1 GI:7995193
GSS; genome survey sequence.
Tetraodon nigroviridis.
SM Tetraodon nigroviridis.
SM Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
E 1 (bases 1 to 953)
S Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottler, F.,
Saurin, W. and Weissenbach, J.
     A2648763 2M0149H21
B0692893 pt08d12.y
A0450340 b001010404
BJ365887 bJ365887
A0319355 RPC111-97
AL340430 Tetraodon
BQ693146 pt11e07.y
AW34296 SJ3111 AG
BH56105 BOGYU25TF
BH45731 B01MV11TF
BH41970 BOHHD54TR
BH289798 BOGEY06TR
BH286798 BOGEY06TR
BH157695 ENTRM27TF
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BH157697 THANATTF
BH157697 THANATTF
BH157697 THANATTF
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BH668214 BOMIF10TR
BG41984 GA_Ea001
AL217092 Tetracdon
BG033546 G02302157
B1883362 ZFG37-2-0
AQ005284 CIT-HSP-2
B541G4 CIT-HSP-2
B541G4 CIT-HSP-2
AV559105 AV559105
AW464877 BP230017A
                                                                                                                                                                                                                                                                                                                                                                                      CNSO43LN
Tetraodon nigroviridis genome survey sequence PUC-Orl end of clone O70NO2 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                 BH741995 gt40d01.9
A1726715 BNLGH1642
A1729966 BNLGH1582
AL446771 Parameciu
AQ662080 HS_2093_B
A1730796 BNLGH1796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 953)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                           PT022K01R
AQ662080
AI730796
AZ883204
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AQ005284
B54164
AV559105
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AW334296
BH752639
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BH536105
BH59790
BH597970
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BH597970
BH741995
AN729966
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CNS02WI3
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BG033546
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117
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Unpublished
sequence.
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222.4
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22.4
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CNSO43LN/C
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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REFERENCE
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AZ23535 220PbF09
AZ27574 Ciona int
AA677944 zi24h07.s
AL063320 Drosophil
AA101244 zn43b06.s
                                                         23:34:41; Search time 2255 Seconds (without alignments) 229.825 Million cell updates/sec

    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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Maximum Match 100%
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AZ523535
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em_gss_pro:*
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Post-processing:

Database

Minimum DB s Maximum DB s

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Characerization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Unpublished

JOURNAL

TITLE

17

23.6 23.2 23.2 22.8 22.8

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Score

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Result

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GSS 03-DEC-2000
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1 (bases 1 to 700)
Simmen,M.W., Leitgeb,S., Clark,V.H., Jones,S.J. and Bird,A.
Gene number in an invertebrate chordate, Ciona intestinalis
Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence analysis of transposable elements in the sea squirt, Ciona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 (bases 1 to 700)
Clark,V.H., Leitgeb,S., Charlton,J., Tweedie,S., Simmen,M.W. and
              œ.
                                                                                                                                                                                                                                                                                           NA linear GSS 03-DEC-
clone 9D10, genomic survey
       vector. Recombinant plasmids were used to transform coli XL10-Gold host cells. " 65\ c 42\ g 226\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 700)
Simmen,M.W., Leitgeb,S., Charlton,J., Jones,S.J., Harris,B.R.,
Clark,V.H. and Bird,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (28-FEB-1998) ICMB, University of Edinburgh, King's Bulldings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact: VCLARK@SEVO.bio.ed.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nonmethylated transposable elements and methylated genes in a chordate genome Science 283 (5405), 1164-1167 (1999)
                                                                                                                                       Gaps
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                                                                                                  Length
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                                                                                                  DB 17;
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89.3%; Pred. No. 1.9e+02;
... n. Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Evol. 17 (11), 1685-1694 (2000)
                                                                                               Score 23.6; DB 17
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Ciona intestinalis"
/db_xref="taxon:7719"
                                                                                                                                                                                                                                                                                                              Ciona intestinalis genomic fragment,
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                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              GSS; genome survey sequence.
Clona intestinalis.
Clona intestinalis
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105 c 115 q
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                                                                                                                                                                                                                                                                                                                                                                   GI:2951400
                                                                                             73.8%;
86.7%;
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                                                                                                                                   26; Conservative
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AJ227574.1
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Matches 25; Conserv
                                           177 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bird, A.P.
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TITLE
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JOURNAL
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CI9D10/c
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                                                                   This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers

1. 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ523535 510 bp DNA linear GSS 07-MAY-2001
220PbF09 Pb MBN #21 Plasmodium berghei genomic 3', DNA sequence.
AZ523535
AZ523535.1 GI:13962603
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/strain="ANKA clone 15cyl (clone of the ANKA 8417 clone)"
/db_xref="taxon:881"
/clone_lib="Pb MBN #21"
/dev_stage="assvual blood forms"
/lab_host="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                          /organism="Tetraodon nigroviridis"
/db_xref="texon:99883"
/clone="079802"
/clone=lib="G"
/note="Genoscope sequence ID : COBG079DG01SP1-end
                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                         DB 17; Length 953; 98;
                                                                                                                                                                                                                                                                                        5 others
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                                                                                                                                                                                                                                                                                                                                       Score 24; DB 1
Pred. No. 98;
0; Mismatches
                                                                                                                                                                                                                                                                                        238
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Class: shotgun.
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                  Genoscope.
Direct Submission
Submitted (12-APR-2000)
                                                                                                                                                                                                                                                                                                                                    vuery Match 75.0%;
Best Local Similarity 84.4%;
Matches 27; Conservative
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     (bases 1 to 953)
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                                                                                                                                                                                                                                                                                    316
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AZ523535/c
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AUTHORS
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COMMENT
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                                                                       COMMENT
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"Web: www.genoscope.cns.fr)

"Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library or fullers for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukāryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(hassa 1 to 526)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dierrich,N., DuBuque,T., Favello,A., Gish,M., Hawkins,M., Hultman,M., Kucaba,T., Legy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA101244 5187 28-OCT-1996 2043b06.sl Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:550163 3', mRNA sequence.
                                                                                        Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Email: est@waston.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40Ml3 fwd. from Amersham
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/db_xref="texon:7227"
/db_ne="BACR07G09"
/clone="laba"RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22.8; DB 17 Pred. No. 2.6e+02;
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174 g
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65.6%;
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Best Local Similarity 65.67
Matches 21, Conservative
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AA101244
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                                                 EST 19-DEC-1997
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                          zi24h07.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA
clone IMAGE:431773 3', mRNA sequence.
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:431773"
/clone_lib="Soares_fetal_liver_spleen_INFLS_S1"
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Pred. No. 2.3e+02;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AATACAACACAATATTAATTGTGTTGTATTA 32
                                                                                                                        AA677944.1 GI:2658466
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Best Local Similarity 83.9%;
Matches 26; Conservative
                                                                                                                                                                                Homo sapiens
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                                                                                                                                                               human.
RESULT 4
AA677944/C
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                                                             DEFINITION
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JOURNAL
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plasmid inserts
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Mus musculus
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Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret, B. Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
Plate: 325 row: C column: 1
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                       Length 526;
                                                          /db_xref="cDB:3228681"
/db_xref="taxon:9606"
/clone="InMAGE:550163"
/clone=lib="stratagene HeLa cell s3 937216"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_GSSS: Rel-33-325cl.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
Tylz Medical For Genomic Research
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                                                                                                                                                     Score 22.6; DB 9;
Pred. No. 3.2e+02;
0; Mismatches 5;
                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                       390 TAATACAAGCNAATATTAAATGTGTTTTAT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-325C1"
High quality sequence stop: 233.
Location/Qualifiers
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GSS.
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                                                                                                                                                                                                                                                                                                                                       Query Match 70.6%;
Best Local Similarity 83.3%;
Matches 25; Conservative C
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AQ970499
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KEYWORDS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.065 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoR1; Site_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECOR1 sites. The ligation products were transformed into
BH10B electrocompetent cells (BRL Life Technologies).

1 109 c 120 g 120 t thers
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Dunn, D., Aoyadi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
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/clone="UUGC2M0149H21"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                              Length 523;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 3.7e+02;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0149 row: H column: 21
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TAATACAACACAATATTAATTGTGTTGTATTA 32
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High quality sequence stop: 562.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                        70.0%;
81.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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70.0%;
81.2%;
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                                                    Query Match
Best Local Similarity
Matches 26; Conserv
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AQ450340.1
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Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 315 286 1800
Fax: 315 286 1800
Fax: 316 280
Fax: 317 286 1800
Fax: 317 286 1800
Fax: 318 286 280
Fax: 318 280

of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicilin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ692893 584 bp mRNA linear EST 15-JUL-2002 pt08012.yl Trichinella spiralis immature Ll pAMP1 vl Trichinella spiralis cDNA 5' similar to SW:AQP9_HUMAN 043315 AQUAPORIN 9. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotta: Metazoa: Nematoda; Enoplea; Trichocephalida;
Trichinellidae: Trichinella.
1 (bases 1 to 584)
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Glbbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Magnire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Staffar,J., Allen,M., Schurk,R., Kohn,S., Staffar,J., McCann,R., Waterston,R., and
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The library was constructed by Claire Murphy and Dr. James
McCarter at Washington University, St. Louis. The CDNA was
made by using Dynabead oligo-dT priming (Dynal). PCR based
library using a modified protocol from the SMART PCR CDNA
Synthesis Kit from Clontech. Directionally cloned into the
UDG sites of pAMP1. Newborn larvae were collected from
infected rats and provided by Dr. Judith Appleton of
Cornell University, Ithaca, NY (jaa2@cornell.edu)."
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/organism="Trichinella spiralis"
/db_xref="taxon:6334"
/db_mrichinella spiralis immature L1 pAMP1 v1"
/dev_stage="Immature L1"
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                                                                                                                                                                                                                                                                                                                                                    Length 562;
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Pred. No. 3.7e+02;
); Mismatches 6;
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81.2%;
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Trichinella spiralis
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//clone_lib="Cplowani3mpl8gbNal"
//lone_lib="Cplowani3mpl8gbNal"
//lone_host="E. coli pnl25"
//note="Vector: M13mpl8 : Site_l: Hind III; C. parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a tight size distribution between 1.5 and 3 kb. Adaptors (pGTAGTCACAACAACTAGTOR) were ligated to the randomly sheared gbNA fragments and pAGTGTTTG linkers were ligated to the Hind III-cleaved M13mpl8 vector. The adaptor-containing inserts were annealed and ligated to the vector and transformed into E. coli strain DH125. Recombinant phagemid clones from the first plating of the library were randomly selected for sequence analysis using the M13(-21) forward primer."
                                                                                                                                                                                                                                                                                                         AQ450340 633 bp DNA linear GSS 08-APR-1999 500010F04.x1 CpIONAM13mp18gDNA1 Cryptosporidium parvum genomic, DNA
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: hyman@sequence.stanford.edu
For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html
Seq primer: M13(-21) forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Alveolata: Apicomplexa; Coccidia; Eimeriida; Cryptosporidiidae; Cryptosporidium.

(Cryptosporidiidae; Cryptosporidium.

(Cryptosporidium parvum genome sequencing demonstration project Cryptosporidium parvum genome sequencing demonstration project Contact: Hyman, R. W.

Stanford DNA Sequencing and Technology Center Stanford University School of Medicine, Palo Alto
855 California Avenue, Palo Alto, CA 94304, USA
Tel: 650 812 1975
                                                                   Gaps
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           Length 584;
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                                                                Indels
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        DB 14;
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81.2%; Pred. No. 3.7e+02;
live 0; Mismatches 6;
Score 22.4; DB 14
Pred. No. 3.7e+02;
                                                          0; Mismatches
                                                                                                                                             1 TAATACAACACAATATTAATTGTGTTGTTA 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="IOWA"
/db_xref="taxon:5807"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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0;

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Indels

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Mismatches

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Conservative
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Best Local Similarity
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AQ319355.1
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25;
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DEFINITION
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                                                                                                                                                 DEFINITION
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JOURNAL
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AUTHORS
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AQ319355
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 Matches
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SOURCE
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AV385246.1 GI:6130303
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                              Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1.239
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="texon:4469"
/clone="dd56024"
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                                            Eukaryota: Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 239)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Halocynthia roretzi"
/db_xref="taxon:7729"
/clone="105A082"
/clone_lib="Halocynthia roretzi Fertilized egg"
/dev_stage="Fertilized egg"
/note="Organ: embryo"
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0
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Eukaryota: Metazoa: Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
I (bases 1 to 505)
Makabe, K.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halocynthia roretzi EST
Unpublished (1999)
Contact: Kazuhiro W. Makabe
Department of Zoology, Graduate School of Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                 1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: kwmakabe@ascidian.zool.kyoto-u.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 22; DB 13; I
Pred. No. 5.3e+02;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22; DB 10;
Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                                         /sex="mat A"
/dev_stage="Culmination stage" .
26 c 1 g 99 t
                                                                                                                            Unpublished (2002)
Context: Tadasus Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sākyo-ku, Kyōtō, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 t
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                    Dictyostelium discoideum. Dictyostelium discoideum
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83.3%;
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83.3%;
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Best Local Similarity
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Best Local Similarity
                                                                                                                 stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
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TITLE
JOURNAL
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AV385246
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                                                                 REFERENCE
AUTHORS
TITLE
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CNSO5JO5

1042 bp DNA linear GSS 26-MAY-2000
Tetraodon nigroviridis genome survey sequence SP6 end of clone
017F15 of library B from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                         AQ319355 STO DNA linear GSS 06-MAY-1999
RPCIII-97J9.TJ RPCI-11 HOMO Sapiens genomic clone RPCI-11-97J9, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)

Unpublished (1998)

Cother_GSSS: RPCIII-97J9.TV

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0208

Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: hbeetigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library availability, please context feter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:737088"
/db_xref="Laxon:9606"
/dlone="RPCI-11-9709"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAGe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBAGe3.6; Site_1"

RPCI1 Human Male BAC Library"
a 88 c 100 g 186 t
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83.3%; Pred. No. 5.2e+02;
.ive 0; Mismatches 5; Indels
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                                   299 TCAAACATAACAATATTAATTGTGTTATAT 328
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1 TAATACAACACAATATTAATTGTGTTAT 30
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AL340430.1 GI:8234188
ACS: genome survey sequence.
Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                               GI:4052320
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Class: BAC ends
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VERSION
KEYWORDS
SOURCE
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Search completed: February 13, 2003, 03:17:52 Job time : 2259 secs
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                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ693146 536 bp mRNA linear EST 15-JUL-2002 ptlle07.yl Trichinella spiralis immature L1 pAMP1 v1 Trichinella spiralis cDNA 5' similar to SW:EF1A_ONCVO P27592 ELONGATION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

[ (bases l to 1042)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                         Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                          2 (bases 1 to 1042)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                      Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-FGenoscope sequence ID : COAB017CC08B1~end : SP6"
213 c 219 g 282 t 31 others
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Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida;
Trichinellidae; Trichinella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21.8; DB 17; Length 1042;
Pred: No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Washington Univ. Nematode EST Project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="017F15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-ALPHA; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-APR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ693146.1 GI:21818462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="B
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1 Similarity 92.0%;
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trichinella spiralis.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 1042)
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Contact: McCarter JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1042
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Best Local Similarity
                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
COMMENT
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REFERENCE
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BQ693146
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AUTHORS
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KEYWORDS
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/organism="Trichinella spiralis"
/db_xref="taxon:6334"
/cloo=llb="Trichinella spiralis immature Ll pAMPl vl"
/dev_stage="immature Ll"
/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="NetCr: pAMPl (Gibco); Site_l: NotI; Site_2: SalI;
/note="Vector: pAMPl Cibco; Discretion of Content of Discretion of Content of Discretion of Content of Discretionally cloned into the UDG sites of pAMPl. Newborn larvae were collected from infected rats and provided by Dr. Judith Appleton of Cornell University, Ithaca, NY (jaa2@cornell.edu)."
Tel: 314 286 1800

Fax: 314 286 1800

Email: estGeatson.wustl.edu

Email: estGeatson.wustl.edu

The library was constructed by Claire Murphy and Dr. James McCarter

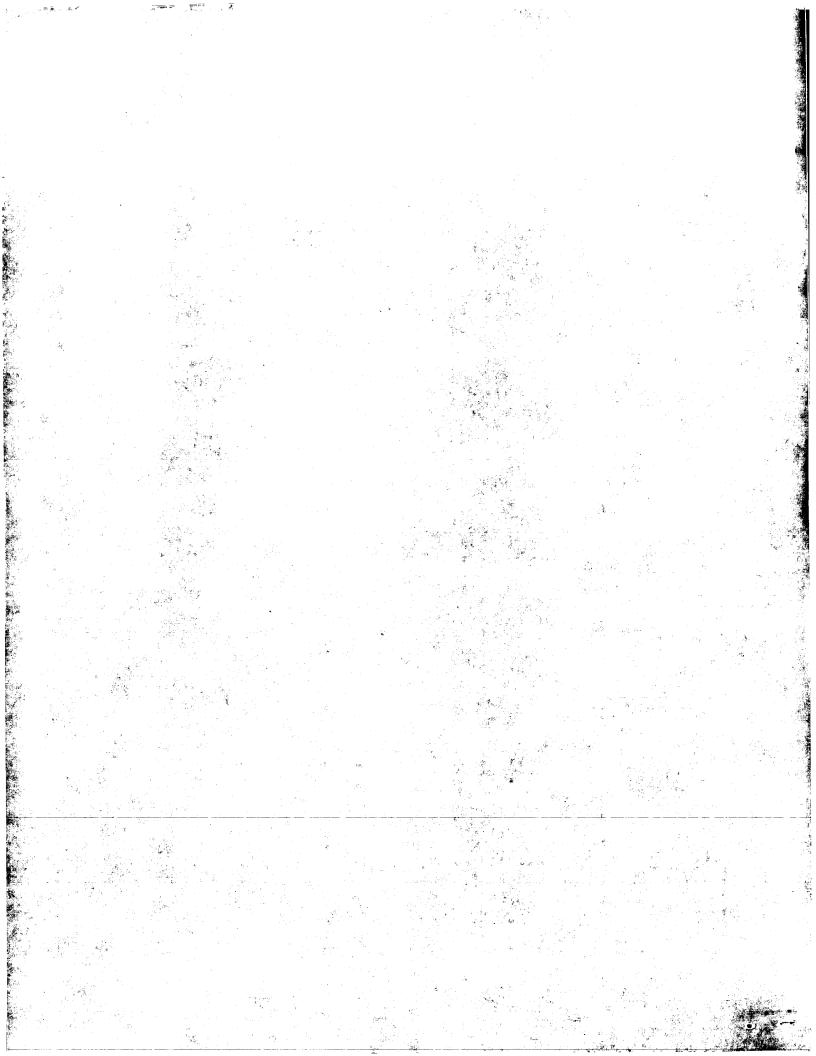
at Washington University, St. Louis. Newborn larvae were collected

from infected rats and provided by Dr. Judith Appleton of Cornell

University, Ithaca. NY (jaa2@cornell.edu).

Seq primer: -40RP from Gibco

High quality sequence stop: 414.
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Pred. No. 7.2e+02;
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85.7%;
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Best Local Similarity 85.7
Matches 24; Conservative
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February 13, 2003, 01:45:51 ; Search time 298 Seconds
    (without alignments)
    1881.703 Million cell updates/sec
                                                                                                                                                                                                                                             1 ggggtaccgccagcatttcg......gacgcggaggaaatcacatg 249
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                 2185239 seqs, 1125999159 residues
                                                                       OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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A. Sindia and J. Malda and J. M N_Geneseq_101002:* 110... 111... 112... 114... 114... 114... 116... 11 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	PKS90 TIR coupling PTREX1 mutant beta Nucleotide sequenc PTREX1A mutant bet Plasmid PTIMTRF1. Nucleotide sequenc Nucleotide sequenc Nucleotide sequenc Enterococcus faeca
SUMMARIES	0 AAX07548 1 AAA15041 1 AAA15041 2 AAX29550 2 AAF29646 1 AAA15043 1 AAA15042 1 AAA15042 2 AAX13472
DB	20 20 21 22 22 21 21 21 21
% Query Match Length DB ID	5230 5230 5230 5231 5231 5497 5497 5870 5870 5906
* Query Match	15.33 15.33 15.33 15.33 15.33 15.33 15.33
Score	38 38 38 38 38 38 38
ult No.	126450786
Result No.	0000000

ALIGNMENTS

RESULT 1

Beta-toxin, cpb; vaccine; infection; protection; retained immunogenicity; haemorragic enteritis; necrotic enteritis; enterotoxemia; lamb dysenteria; translation initiation region; ds. Wells JM; Waterfield NR, AAX07548/c ID AAX07548 standard; DNA; 5216 BP. Sergers RPAM, 98EP-0202032. 97EP-0201888. (first entry) pKS90 TIR coupling vector. (ALKU) AKZO NOBEL NV. WPI; 1999-083571/08. Frandsen PL, 08-JUN-1999 17-JUN-1998; 20-JUN-1997; EP892054-A1 20-JAN-1999 Synthetic. AAX07548;

New detoxified derivative of Clostridium perfringens beta-toxin - with retained immunogenicity, useful as a vaccine to protect against

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GGGGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAG 38
                                                                                                                                                                                                                                                                                                                                                         AAA15041;
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AAA15041/c
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SSSXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New detoxified derivative of Clostridium perfringens beta-toxin with retained immunogenicity, useful as a vaccine to protect against Clostridium perfringens infection
                                                                    The sequence is that of the vector pKS90 which was used in the construction of a detoxified immunogenic derivative of Clostridium perfiringens beta-toxin. Such a derivative is useful as a vaccine to induce an immune is more an appropriate and protect against Clostridium perfringens infection in man, pig, lamb, sheep, goat, calf and bird, which causes haemorragic enteritis, necrotic enteritis, enteritis, enteritis, and enterotoxemia and lamb dysenteria. The new beta-toxin has been detoxified without impalring the immunogenicity, unlike prior art vaccines which used chemical and formalin detoxifying methods. Production of the beta-toxin in gram positive bacteria prevents prior art difficulties of isolation from dangerous Clostridium perfringens, and purification from the Clostridium perfringen spores.
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta-toxin; cpb; vaccine; infection; protection; retained immunogenicity; haemorragic enteritis; necrotic enteritis; enterotoxemia; lamb dysenteria; ds.
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                                                                                                                                                                                                                                                                                                                                                           Length 5216;
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                                                                                                                                                                                                                                                                                                                        Sequence 5216 BP; 1934 A; 790 C; 980 G; 1512 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wells JM;
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2.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pTREX1 mutant beta-toxin expression cassette.
                                                                                                                                                                                                                                                                                                                                                 15.3%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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     Clostridium perfringens infection
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                                           Example; Fig 2b; 30pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                      38; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-1998;
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AAX07549/
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Production of the beta-toxin in gram positive bacteria prevents prior art difficulties of isolation from dangerous Clostridium perfringens, and purification from the Clostridium perfringen spores.
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Intestinal mucosa; cytokine; cytokine antagonist; anti-inflammatory; Gram-positive bacteria; Lactococcus lactis; gastrointestinal tract; inflammatory bowel disease; chronic colitis; Crohn's disease; IL10; ulcerative colitis; tumour necrosis factor; TNF; interleukin 10; ss.
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                                                                                                                        Sequence 5230 BP; 1930 A; 795 C; 983 G; 1522 T; 0 other;
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ilarity 100.0%; Pred. No. 2.9e-08;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                            DB 20; L
2.9e-08;
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                                                                                                                                                                                                                                                                                                                                                            2323 GGGGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAG 2286
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                                                                                                                                                                         15.3%; Scc...
100.0%; Pred. No. ...
... 0; Mismatches
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Best Local Similarity 100.0
Matches 38; Conservative
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Best Local Similarity
Matches 38; Conserv
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08-JUN-1999

AAX07550;

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The present sequence is a recombinant vector which may be used to generate a recombinant Lactococcus lactis capable of delivering a trefoil peptide in vivo. The recombinant microorganism is useful for computed in vivo. The recombinant microorganism is useful for manufacturing an agent for the delivery of a trefoil peptide to the gastrointestinal tract, and for treating sastric or intestinal diseases or of disorders, or lesions caused by gastric or intestinal diseases or constructs. The microorganism may also be used for preparing medicament to be used for treating gastric and vor gastrointestinal diseases or colitis, acute flare useps of Crohn's diseases, or ulcerative colitis, acute flare useps of Crohn's diseases, or ulcerative colitis, acute flare useps of Crohn's diseases of the gastrointestinal connections of disease states which can be treated by the colitis colitis ulcerosa). Disease states which can be treated by the method or compositions comprising the recombinant microorganism or trefoil peptides include disorders of and damage to the alimentary canal, cas well as for the protection and treatment of tissues that lie outside the animantary canal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant Lactococcus lactis for delivering a trefoil peptide useful for treating acute or chronic gastrointestinal inflammatory diseases or disorders, e.g. acute or ulcerative colitis, acute flare-ups of Crohn's
                                         Mouse TFF1; mTFF; trefoil protein; antiinflammatory; gastrointestinal; anti-ulcer; peptide therapy; gastrointestinal disease; acute colitis; Crohn's disease; ulcerative colitis; plasmid primTFF1; recombinant vector; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Intestinal mucosa; cytokine; cytokine antagonist; anti-inflammatory; Gram-positive bacteria; Lactococcus lactis; gastrointestinal tract; inflammatory bowel disease; chronic colitis; Crohn's disease; IL10; ulcerative colitis; tumour necrosis factor; TNF; interleukin 10; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5497 BP; 1994 A; 870 C; 1051 G; 1582 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of expression plasmid pTlMIL10.
                                                                                                                                                                                                                                                                                                                                                       (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; I
2.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2590 GGGGTACCGCCAGCATTCGGAAAAAAACCACGCTAAG 2553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGGGTACCGCCAGCATTTCGGAAAAAACCACGCTAAG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.3%; Score 38; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                          Remaut ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 18; Fig 1c; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA15043/c
ID AAA15043 standard; DNA; 5770 BP.
                                                                                                                                                                                                                                                                      05-JUL-2000; 2000WO-EP06343
                                                                                                                                                                                                                                                                                                                    99EP-0870143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Steidler L,
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-138142/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 38; Conserv
                                                                                                                                                                                      WO200102570-A1
                                                                                                                                                                                                                                                                                                                  05-JUL-1999;
                                                                                                                                                                                                                                  11-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-2000
                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                     Hans WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA15043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of the pTREXIA expression cassette which was used in the construction of a detoxified immunogenic derivative of Clostridium perfringens beta-toxin. Such a derivative is useful as a vaccine to induce an immune response and protect against Clostridium perfringens infection in man, pig, lamb, sheep, goat, calf and bird, which causes haemorragic enteritis, necrotic enteritis, enterotoxemia and lamb dysenteria. The new beta-toxin has been art vaccines which used chemical and formalin detoxifying methods. Production of the beta-toxin in gram positive bacteria prevents prior art difficulties of isolation from dangerous Clostridium perfringens, and purification from the Clostridium perfringen spores.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New detoxified derivative of Clostridium perfringens beta-toxin - with retained immunogenicity, useful as a vaccine to protect against Clostridium perfringens infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                            Beta-toxin, cpb, vaccine; infection; protection; retained immunogenicity; haemorragic enteritis; necrotic enteritis; enterotoxemia; lamb dysenteria; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wells JM;
2323 GGGGTACCGCCAGCATTCGGAAAAAACCACGCTAAG 2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterfield NR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Fig 1b; 30pp; English
                                                                                                     AAX07550/c
ID AAX07550 standard; DNA; 5231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
AAF29646/c
ID AAF29646 standard; DNA; 5497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sergers RPAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98EP-0202032
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                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALKU ) AKZO NOBEL NV.
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Frandsen PL,

17-JUN-1998; 20-JUN-1997;

EP892054-A1 20-JAN-1999

Synthetic.

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Gaps

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10-APR-2001

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AAF29646;

Query Match

Matches Н

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(VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA15042/c
ID AAA15042 standard; DNA; 5906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-EP07800
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                                    Remaut ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-422481/36.
                                                                    WPI; 2000-422481/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200023471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-0CT-1998;
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                                      Steidler L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
          0;
                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents an expression plasmid for use in the course of the invention. The specification describes an administration strategy for the delivery at the intestinal nuccosa of cytokines or cytokine antagonists, preferably of acid sensitive anti-inflammatory agents such as interleukin 10 (ILIO) or tumour necrosis factor (TNF). The method uses a cytokine-producing or cytokine antagonist-producing Gram-positive bacterial strain (such as Lactococcus lactis). The use on-colonizing bacterial strain (such as Lactococcus lactis). The use form-positive bacterial expressing cytokines or cytokine antagonists allows the treatment to be directed to the disease site, whilst tract. The recombinant bacteria are used in the treatment of inflammatory bowel diseases, especially chronic collits, Crohn's disease or an increasing collits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Intestinal mucosa; cytokine; cytokine antagonist; anti-inflammatory; Gram-positive bacteria; Lactococcus lactis; gastrointestinal tract; inflammatory bowel disease; chronic colitis; Crohn's disease; IL10; ulcerative colitis; tumour necrosis factor; TNF; interleukin 10; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                      Ø
                                                                                                                                                                                                                                                                                 Treating inflammatory bowel diseases comprises administering composition comprising a cytokine-producing or cytokine antagonist-producing Gram-positive bacterial strain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5770 BP; 2092 A; 922 C; 1109 G; 1647 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of expression plasmid pTlTR5AH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               score 38; DB 21; I
; Pred. No. 2.9e-08;
0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2863 GGGGTACCGCCAGCATTCGGAAAAAACCACGCTAAG 2826
                                                                                                                                                                                        (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGGGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.3%; Score 38; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1C; 45pp; English.
                                                                                                                                                                                                                           Fiers W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA15044/c
ID AAA15044 standard; DNA; 5870
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                                                                                                                               99WO-EP07800.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 38; Conservative
                                                                                                                                                                                                                           Remaut ER,
                                                                                                                                                                                                                                                          WPI; 2000-422481/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ulcerative colitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200023471-A2
                                                                 WO200023471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-2000.
                                                                                                                                 06-OCT-1999;
                                                                                                                                                               20-0CT-1998;
                                                                                                                                                                                                                             Steidler L,
                                                                                                   27-APR-2000
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                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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The present sequence represents an expression plasmid for use in the course of the invention. The specification describes an administration strategy for the delivery at the intestinal nucosa of cytokines or cytokine antagonists, preferably of acid sensitive anti-inflammatory agents such as interleukin 10 (ILIO) or tumour necrosis factor (TNF). The method uses a cytokine-producing or cytokine antagonist-producing Gram-positive bacterial strain (such as Lactococcus lactis). The use of non-colonizing bacterial strain (such as Lactococcus lactis). The use of mon-colonizing bacteria expressing cytokines or cytokine antagonists allows the treatment to be directed to the disease site, whilst tract. The recombinant bacteria are used in the treatment of inflammatory bowel diseases, especially chronic colitis, Crohn's disease or an ulcerative colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Intestinal mucosa; cytokine; cytokine antagonist; anti-inflammatory; Gram-positive bacteria; Lactococcus lactis; gastrointestinal tract; inflammatory bowel disease; chronic colitis; Crohn's disease; IL10; ulcerative colitis; tumour necrosis factor; TNF; interleukin 10; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                              Treating inflammatory bowel diseases comprises administering a composition comprising a cytokine-producing or cytokine antagonist-producing Gram-positive bacterial strain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating inflammatory bowel diseases comprises administering composition comprising a cytokine-producing or cytokine antagonist-producing Gram-positive bacterial strain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5870 BP; 2097 A; 960 C; 1142 G; 1671 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.3%; Score 38; DB 21; 100.0%; Pred. No. 2.9e-08; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2963 GGGGTACCGCCAGCATTTCGGAAAAAACCACGCTAAG 2926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ilarity 100.0%; Pred. No. 2.5
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 1C; 45pp; English.
Fiers W;
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Gaps

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inflammatory
course of the invention. The specification describes an administration strategy for the delivery at the intestinal mucosa of sytokines or cytokine antagonists, preferably of acid sensitive anti-inflammatory agents such as interleukin 10 (ILMO) or tumour necrosis factor (TNF). Gram-positive bacterial strain (Such as Lactococcus lactis). The use of aniomizing bacterial strain (Such as Lactococcus lactis). The use of allows the treatment to be directed to the diseases site, whilst minimizing the possibility of degradation along the gastrointestinal bowel diseases, especially chronic colitis, Crohn's disease or an ulcerative colitis.
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Gaps 0; Length 5906; Sequence 5906 BP; 2204 A; 932 C; 1130 G; 1640 T; 0 other; Indels DB 21; I 2.9e-08; 21; 1 GGGGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAG 38 15.3%; Score 38; DB 100.0%; Pred. No. 2.9 tive 0; Mismatches Best Local Similarity 100. Matches 38; Conservative Query Match 2999 g ð

; 0

Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds. Enterococcus faecalis genome contig SEQ ID NO:535 AAX13472 standard; DNA; 1566 (first entry) 19-MAR-1999 AAX13472; RESULT

97US-0066009. 97US-0044031. 97US-0046655. 98WO-US08985 04-MAY-1998; 14-NOV-1997; 06-MAY-1997; 16-MAY-1997; 12-NOV-1998

Enterococcus faecalis

WO9850555-A2.

(HUMA-) HUMAN GENOME SCI INC Barash

Dillon PJ, Kunsch CA;

sc,

WPI; 1999-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus

Claim 1; Page 1787-1788; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based commercial importance. The products can be used to detect the presence of Enterococcus faecalis genome with of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to

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modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                            SNP;
                                                                                                    Gaps
                                                                                                                                                                                                                                                           Human: tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism;
                                                                                                                                                                                                                                         Tumour suppressor gene derived chemically modified sequence #386.
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                                                                             Score 19; DB 20; Length 1566;
Pred. No. 21;
0; Mismatches 0; Indels
                                                                                                 Indels
                                                           G; 559 T; 14 other;
                                                       Sequence 1566 BP; 460 A; 273 C; 260
                                                                             7.0°,
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin K;
                                                                                                                                                                                   BP.
                                                                                                                           1489 TTTTTATACAAAAATAAT 1507
                                                                                                                                                                                AAS46664 standard; DNA; 6076
                                                                                                                98 TTTTTATACAAAAATAAT 116
                                                                                                                                                                                                                                                                                                                                                        15-MAR-2001; 2001WO-EP02955.
                                                                                                                                                                                                                                                                                                                                                                                     2000DE-1019058.
2000DE-1019173.
                                                                                                                                                                                                                                                                                                                                                                                                         2000DE-1032529.
2000DE-1043826.
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                                                                                               19; Conservative
                                                                                                                                                                                                                                                                                cytosine methylation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piepenbrock
                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             07-APR-2000;
30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                           15-MAR-2000;
06-APR-2000;
                                                                                                                                                                                                                                                                                                                                       20-SEP-2001
                                      infection
                                                                                                                                                                                                   AAS46664;
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                                                                                             Matches
                                                                                                                                                              RESULT 10
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and concogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences.

(Ss) and sequences complementry to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may complemented polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. array for analysing diseases associated with CpG dinucleotides e.g. ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific ciseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters may be

Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.

Claim 1; SEQ ID No 386; 27pp; English.

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Matches
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differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID), ID 536 and ID 535, except for those whose partner sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour;
cytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1;
UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
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                                                                                                                                               ID 2 and ID1, in journment is missing).

Is missing).

Note: The sequence data for this patent did not form part.

Note: The specification, but was obtained in electronic fire printed specification, but was obtained in electronic format directly from NIPO at
                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 6076;
20;
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                 Sequence 6076 BP; 2013 A; 73 C; 1223 G; 2767 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human chemically pretreated gene sequence #62 strand 2.
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
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                                                                                                                                                                                                                                                                                                                                                             7.6%; Scc.
100.0%; Pre
0; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3018 AAATAATACAACACAATA 3000
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01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 AAAATAATACAACACAATA 127
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                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK40042;
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Matches
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 558 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (SS) and sequences complementary to (SS). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state
which hybridises to or is identical to a chemically pretreated DNA of genes associated with pharmacogenomics and their complements, arranged in an array for analysing diseases associated with the methylation state (CpG) and/or detecting SNPs (single nucleotide polymorphisms) of the 87 sequences. The oligomers may also be used as PCR primers. The set of 87 nucleic acids and their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence represents one the 87 DNA sequences or its complement.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP; cytosine methylation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour suppressor gene derived chemically modified sequence #253.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6136;
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6136 BP; 1775 A; 69 C; 1285 G; 3007 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19;
Pred. No.
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100.08; Pre-
0;
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07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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Homo sapiens.
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and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the arrange of the arrange of the time of the time tumour suppressor genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHIP; Pleckstrin homology domain-interacting protein; NDRP; ds; deuconal differentiation-related protein; insulin receptor substrate; IRS; signal transducer and activator of transcription; STAT; transgent animal; diabetes mellitus type 2; hyperglycaemia; myotonic muscular dystrophy; acanthosis; nigricans; retinopathy; nephropathy; artherosclarosis; peripheral arterial disases; ancer; adenocarcinoma; leukaemia; breast cancer; prostate cancer; colon cancer; ovarian cancer; autoimmune disease; inflammation; immunodeficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 7008; 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                   ftp.w1po.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                              Score 19;
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Matches 19; Conservative
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(FARH/) FARHANG-FALLAH
(CHEN/) CHENG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-041586/05.
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                                                                                                                                                                                                                           oncogenes.
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AAS98600/c
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insulin

The invention relates to an isolated Pleckstrin homology domain interacting protein (PHIP) that recruits proteins of the insulir

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Transcription (STAT) transcription factors, to receptors that interact with and phosphorylate the proteins and STAT transcription factors, the nucleic acid encoding PHIP (nPHIP), a nucleic acid which binds to nPHIP or regions of it, analogues, fragments or allelic variants of PHIP or nPHIP, a nucleic acid sequence faving substantial sequence identity or or nPHIP, a nucleic acid sequence fully defined or nPHIP in another acid sequence fully defined them neuronal differentiation-related protein (NDRP) nucleic acid sequence or its exons as given in the specification, expression cannot be already expressing PHIP. The nucleic acids, proteins and antibodies are useful for diagnosis and treatment of a condition associated with an insulin receptor (e.g. diabbetes mallitus caids, proteins and antibodies are useful for diagnosis, peripheral acondition associated with an insulin receptor (e.g. diabbetes mallitus carefusly reproperty, nephropathy, netheroscierosis, peripheral arterial disease) or cancer (e.g. adenocarcinoma, leukaemia, breast cancer, prostate cancer, colon cancer, ovarian cancer and many others cancer, prostate cancer, colon cancer, ovarian cancer and many others cancer, prostate cancer, colon cancer, ovarian cancer and many others cancer, prostate cancer, colon cancer ovarian cancer and many others cancer, prostate cancer, colon cancer, ovarian cancer and many others cancer inmune disease, inflammation and immunodeficiency. The protein is also useful for discovering cunction. The present sequence is genomic DNA encoding PHIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed sequence tag; secreted protein; cDNA isolation;
tor substrate (IRS) family, and signal transducer and activator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 140036 BP; 48500 A; 25843 C; 22499 G; 43194 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.6%; Score 19; DB 24; Length 140036;
100.0%; Pred. No. 17;
-ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein 5' EST, SEQ ID NO: 26729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 26729; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 128998 AGTTAAAAATCAGAAAT 128980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC22654 standard; cDNA; 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage

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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABM15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
                                                                                                                                                                                                                                                                                                                      ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating CDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length CDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                      ·,
                                                                                                                                                                                                                                                                         Score 18; DB 21; Length 251;
Pred. No. 68;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ORFX polynucleotide sequence SEQ ID NO:1883.
                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                               Sequence 251 BP; 92 A; 38 C; 52 G; 69 T; 0 other;
                                                                                                                                                                                                                                                                                     100.0%; Pred. w.---ive 0; Mismatches
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                                                                                                                                                                                     expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABN16703 standard; cDNA; 286 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-2001; 2001WO-US10836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myasthenia gravis; gene; ss
                                                                                                                                                                                                                                                                                                                                                                    137 TIGTATTAGGTGTTATAA 154
                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                            Query Match 7.2%
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimkets RA, Leach MD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-106308/14.
P-PSDB; ABP00951.
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transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hyperthemsion, hypethyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune thyroiditis, myasthenia gravis, rheumatoid arthitis, autoimmune inflammatory eve disease. OREX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.

Systemic cytokine damage.

Specification, but was obtained in electronic format directly from WIPO
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0
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 286 BP; 77 A; 71 C; 58 G; 80 T; 0 other;
                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: February 13, 2003, 04:59:25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 TTTTTTATACAAAAATA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
nes 18; Conservative
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us-09-895-435-4.rni

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Sequence 3, Application US/09330611
Patent No. 6248874
GENERAL INFORMATION:
APPLICANT: FREY, Perry A.
APPLICANT: RUZICKA, Frank J.
TITLE OF INVENTION: DNA MOLECULES ENCODING BACTERIAL LYSINE 2,3-AMINOMUTASE
FILE REFREENCE: 032026/0476
CURRENT APPLICATION NUMBER: US/09/330,611
EARLIER APPLICATION NUMBER: US 09/198,942
EARLIER FILING DATE: 1999-106-11
EARLIER FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
                                                                                                             February 13, 2003, 04:52:47 ; Search time 67 Seconds
(without alignments)
1139.739 Million cell updates/sec
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1, Appli
2403, Ap
2149, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 9999taccgccagcatttcg.....gacgcggaggaaatcacatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_NA:*
1: /cgn2_6/ptcdata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptcdata/2/ina/FB_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-858-207A-174
US-08-961-527-193
US-07-593-657-6
US-08-942-0128-3
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US-09-134-001C-2149
US-07-593-657-14
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US-08-449-315-36
US-08-449-043-36
US-08-456-265A-36
US-08-455-244-36
US-08-455-244-36
US-08-455-244-36
US-08-455-240-36
US-08-456-262-36
US-08-456-262-36
US-08-456-262-36
US-08-456-262-36
US-08-456-240-36
US-08-456-240-36
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US-08-456-240-36
US-08-456-240-36
US-08-456-240-36
US-08-456-240-36
US-08-456-240-36
US-09-350-600-36
US-09-350-600-36
US-09-318-448-11
                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Listing first 45 summaries
                                                                          · nucleic search, using sw model
                                                                                                                                                                                                                                                                                     OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                          OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
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                                                                                                                 Run on:
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JMBER: US 08/042,847
6-APR-1993
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Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD 11018 AAAAAATCAGAAAATAT 11002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFA: (919)541-8689
INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS:
LENGTH: 12124 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 AAAAATCAGAAAATAT 67
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 6-APR-195
PRIOR APPLICATION NUMBER: US
FILING DATE: 21-DEC-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; IMMEDIATE SOURCE;
; CLONE: pBScucchrcht5
US-08-181-271A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Ryals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                          ;
0
                                                                                                                                                    Length 1029;
                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,271A FILING DATE: 1.3AN-94 CLASSIFICATION: 435
                                                                                                                                                    Score 17; DB 4;
Pred. No. 18;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-ARR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
ZUOUNTRY: USA
ZIP: 10532
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APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                    Sequence 36, Application US/08181271A Patent No. 5614395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                       Ryals, John A.
Alexander, Danny C.
Beck, James J.
Puesing, John H.
Friedrich, Leslie B.
                                                                                                                                             6.8%; SCC.
100.0%; Pre
0;
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Stinson, Jeffrey R.
Uknes, Scott J.
Ward, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
                                                                                                                                                                                                                            226 TATAGACGCGGAGGAAA 242
                                                                                                                                                                                                                                                    102 TATAGACGCGGAGGAAA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 13-JAN-94
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US
FILING DATE: 16-JUL-19
                                             ORGANISM: Escherichia coli FEATURE:
                                                                                                                                                            Query Match 6.8
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                               NAME/KEY: CDS;
LOCATION: (1)..(1026)
US-09-330-611-3
                                                                                                                                                                                                                                                                                                                        RESULT 3
US-08-181-271A-36/c
SEQ ID NO 3
LENGTH: 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                   TYPE: DNA
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Cucumis sativus
INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17; DB 1;
Pred. No. 16;
0; Mismatches (
                                                                                                                                                                                          PRIOR DATE: 27-SEP-1991
PRIOR PAPLICATION NUMBER: US 07/768,122
PRIOR PAPLICATION DATE: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATE: US 07/368,672
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
BATTANG DATE: 13-NAR-1989
PRIOR APPLICATION UNMBER: US 08/045,957
                                                                                PILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/045,957 FILING DATE: 12-APR-1993 ATTORNEY/AGENT INFORMATION:
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
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; Sequence 36, Application US/08449315
; Patent No. 5650505
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"euhaus, Jean-Marc

"APLICANT: Payne, George B.

APPLICANT: Stinson, Jeffrey B.

APPLICANT: Stinson, Jeffrey R.

APPLICANT: Wild, Eric R.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSE CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

STATE: New York

COUNTRY: USA

ZIP: 10532

COMPUTER PT.

WET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRILING DATE: 24-MAY-1995
CLASSIFICATION NUMBER: US/08/449,315
CLASSIFICATION NUMBER: 08/095
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: 08/181,271
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-APR-1991
APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-RER-1993
APPLICATION NUMBER: US 08/042,504
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/88,506
FILING DATE: 20-OCT 1989
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
APPLICATION NUMBER: US 07/580,431
FILING DATE: 37-SEP-1991
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
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FILING DATE: 20-UN-1989
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION UNBER: US 08/045,957
FILING DATE: 12-APR-1983
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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Gaps
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APPLICANT: Ward, Eric R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                     6.8%; Score 17; DB 1; Length 12124;
100.0%; Pred. No. 16;
Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                          ORGANISM: Cucumis sativus
INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
IMMEDIATE SOURCE:
ICONE: pSScucchrcht5
US-08-449-315-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/44.4.0.0.
       S-19825/P1/CGC 1727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CTBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-2NA-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
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Patent No. 5654414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
REFERENCE/DOCKET NUMBER: S-19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ryals, John A.
Alexander, Danny C.
Beck, James J.
                                                                                                                                                       TOPOLGGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                     LENGTH: 12124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                          Db 11018 AAAAAATCAGAAAATAT 11002
                                                                                                                                                                                                                                                                                                                                                                                       51 AAAAATCAGAAAATAT 67
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-444-803-36/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
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APPLICANT:
APPLICANT
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Ward, Eric R.
APPLICANT: Ward, Eric R.
APPLICANT: Wall, Eric R.
APPLICANT: Wall, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,043 FILING DATE: 24 MAY-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APPT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-MAY-1995
CLASSIFICATION 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
FILING DATE: 16-JUL-1993
PRIOR APPLICATION NUMBER: US 08/093,301
FILING DATE: 6-001-1993
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOW-1992
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
APPLICATION NUMBER: US 07/768,122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JMBER: US 07/848,506
6-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                    Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                      Alexander, Danny C.
Beck, James J.
Duesing, John H.
                                                                                                                                                                                                                      Moyer, Mary B.
Neuhaus, Jean-Marc
                Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10532
10532
                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Cucumis sativus
INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 36,129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (410)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.8%; Score 17; DB 3
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/15,566
FILING DATE: 8-MAR-1989
PRIOR APPLICATION DATA: 0-APPLICATION NUMBER: US 07/15,667
FILING DATE: 1-APR-1939
PRIOR APPLICATION DATA: 1980
PRIOR APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION NUMBER: US 07/425,504
FILING DATE: 1-DEC-1990
PRIOR APPLICATION NUMBER: US 07/425,504
FILING DATE: 6-MAR-1992
PRIOR APPLICATION NUMBER: US 07/425,504
FILING DATE: 1-BC-1990
PRIOR APPLICATION NUMBER: US 07/88,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION NUMBER: US 07/768,122
APPLICATION NUMBER: US 07/368,672
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/368,672
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/368,672
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA: TSEP-1993
PRIOR APPLICATION DATA: TSEP-1993
PRIOR APPLICATION DATA: TSEP-1993
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 07/368,672
REGISTERATION NUMBER: 36,130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 12124 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 AAAAATCAGAAAATAT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; CLONE: pBScucchrcht5
US-08-444-803-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:

RESULT 6 US-08-440-043-36/c Sequence 36, Application US/08449043 ; Patent No. 5689044

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6.8%; Score 17; DB 1; Length 12124; 1000.0%; Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Cucumis sativus
INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 16
Mismatches
                                                 FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/678,378
FILING DATE: 1-ARR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1899
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-0CT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/86,122
FILING DATE: 27-SEP-1991
APPLICATION NUMBER: US 07/86,122
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-WAR-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-WAR-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 12-ARR-1983
ATTORNEY/AGENT INFORMATION:
NAME: MAICH INFORMATION:
                               APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
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US-08-455-416-36/c
; Sequence 36, Application US/08455416
; Detent No. 5777200
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-:
TELECOMMUNICATION:
TELEPHONE: (919)541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 12124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 11018 AAAAATCAGAAAATAT 11002
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Best Local Similarity
Matches 17; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
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Patent No. 5767369
GENERAL INFORMATION:
APPLICANT: Alexander, Danny C.
APPLICANT: Ryals, John A.
APPLICANT: Stinson, Jeffrey R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIAA-GEIGY Corporation
STREET: 520 White Plains Road, P.O. Box 2005
STREET: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Cucumis sativus
INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
IMMEDIATE SOURCE:
                                                                            APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEX/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/OFOCKET NUMBER: 36,129
REFERENCE/OFOCKET NUMBER: 36,129
REPROMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEPHONE: (919)541-8614
TELEPHONE: (119)541-8614
TELEPHONE: (119)541-8614
TELEPHONE: (110)541-8614
TYPE: NUMBER: 35,1016
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
FILING DATE: 13-3AN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US/08/456,265P
31-MAY-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 17; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 AAAAAATCAGAAAATAT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE: pBScucchrcht5
US-08-449-043-36
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE: 31-MAY
CLASSIFICATION: 435
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US-08-456-265A-36/c
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Gaps

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APPLICANT: Newlab. John A. APPLICANT: Newlab. John A. APPLICANT: Newlab. John A. APPLICANT: Back, James J. APPLICANT: Redearly. John B. APPLICANT: Marker Main. John Program Handle, John Handle
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Cucumis sativus
INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
IMMEDIATE SOURCE:
CLONE: PBScucchrcht5
US-08-455-416-36
           APPLICATION

FILING DATE: 24-MAR-120.
FILING APPLICATION DATE:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFRENCE/DOCKET NUMBER: 5-19825/P1/CGC 1727
TELEPHOWE: (919)541-8614
TELEPHOWE: (919)541-8614
INFORMATION FRO IN NO: 36:
SEQUENCE CARRACTERISTICS:
LENGTH: 12124 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIBA-GEIGY Corporation
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Montoya, Alice
Moyer, Mary B.
Neuhaus, Jean-Marc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duesing, John H. Friedrich, Leslie B. Goodman, Robert M. Harms, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
Ward, Eric R.
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Alexander, Danny C.
Beck, James J.
                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: New York
IRY: USA
10532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Ne
COUNTRY:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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PatentIn Release #1.0, Version #1.25

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APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 08/093,301
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 07/937,197
FILING DATE: 16-JUL-1993
APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-PR-1991
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-PR-1991
APPLICATION NUMBER: US 07/678,378
FILING DATE: 8-MAR-1988
FILING DATE: 8-MAR-1988
FILING DATE: 8-MAR-1988
FILING DATE: B-MAR-1988
FILING DATE: B-MAR-1988
FILING DATE: B-MAR-1988
FILING DATE: G-TRE-1993
FILING DATE: 1-DATC-1990
FRIOR APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
FRIUNG DATE: 21-DEC-1990
FRIUNG DATE: 20-OCT 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      RESULT 10
US-08-454-876-36/c
; Sequence 36, Application US/08454876
; Patent No. 5804693
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Stinson, Jeffrey R.
Uknes, Scott J.
Ward, Eric R.
                                                                                                                                                                                                                                                                           Ryals, John A.
Alexander, Danny C.
Beck, James J.
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Neuhaus, Jean-Marc
Payne, George B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
: USA
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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6.8%; Score 17; DB 1; Length 12124;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cucumber Chitinase Genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer' James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 3-19825/P1/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8689
INFORMATION FOR SEQ ID NO: 36:
FENENCE CHARACTERISTICS:
CURRENT ABLEATION DATA:

APPLICATION NUMBER: US/08/455,244
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/455,244
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 15-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-NUL-1993
APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-MPR-1991
APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-MPR-1991
APPLICATION NUMBER: US 07/55,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 6-FEB-1999
APPLICATION NUMBER: US 07/632,441
FILING DATE: 6-APR-1993
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 6-MAR-1992
APPLICATION NUMBER: US 07/425,504
FILING DATE: 6-MAR-1992
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INDIVIDUAL ISCLATE: Cucumber
IMMEDIATE SOURCE:
CLONE: PBScucchrcht5
US-08-455-244-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 12124 base pairs
TYPE: nucleic acid
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Gaps

; 0

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COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-19825/P1/CGC 1727
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PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATE:
APPLICATION DATE: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/84,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/84,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION NUMBER: US 07/768,122
FILING DATE: 7-SEP-1991
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
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PRILING LATE:

APPLICATION NUMBER: US 07/368,672

FILING DATE: 20-001-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-WAR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/045,957

FILING DATE: 12-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: BIMER: James Scott

REGISTRATION NUMBER: 36,1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 6-NOV-1992
FILING DATE: 6-NOV-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: 6-APR-1993
                                                                                                                                                                                                                                                                                                                                            FILING DATE: 31-MAY-1995
CLASIFICATION: 800
PRIOR APPLICATION NUMBER: 08/181,271
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-3M-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATE: 16-JUL-1993
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
             ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                  ырык: US/08/457,364
31-MAY-1995
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TELERAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic ac:
STRANDEDNESS: sin
TOPOLOGY: linear
                                    STREET: / o.,
CTTY: Hawthorne
                                                                                               New York
: USA
                                                                                                                                                 10532
                                                                    CITY: Har
STATE: N
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APPLICANT: Ward, Eric R.
APPLICANT: Walliams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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6.8%; Score 17; DB 1; Length 12124;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cucumber Chitinase Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-19825/P1/CGC 1727
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/848,506
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UUN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 20-UUN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APF. US 08/045,957
FILING DATE: 12-APF. 1993
REFERENCE/DOCKET NUMBER: S-19825/PI,
REFERENCE/DOCKET NUMBER: S-19825/PI,
REFERENCE/DOCKET NUMBER: S-1981
TELECOMMUNICATION INDORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 36:
SEQUENCE CHARRCTERISTICS:
TENEMENT. 17124 Dasse pairs
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Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
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Patent No. 5847258
GENERAL INFORMATION:
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Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alexander, Danny C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Cucumis sativus
INDIVIDUAL ISOLATE: Cucumb
IMBDIATE SOURCE:
CLONE: pBScucchrcht5
US-08-454-876-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 11018 AAAAATCAGAAATAT 11002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 12124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AAAAAATCAGAAAATAT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-08-457-364-36/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   υνοΑΝΙΣΜ: Cucumis sativus
; INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA; IMMEDIATE SOURCE:
; CLONE: pBScucchrcht5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727 TELECOMMUNICATION: TELEPHONE: (919)541-8614
                 APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
FILING DATE: 6-MAR-1992
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
APPLICATION NUMBER: US 07/580,431
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 20-UN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 07/369,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAMME: FILING DATE: 12-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alexander, Danny C. Beck, James J. Duesing, John H. Friedrich, Leslie B. Goodman, Robert M. Harms, Christian Meins, Jr., Frederick Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Application US/08456240; Patent No. 5856154
GENERAL INFORMATION:
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100.08; Pre
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REGISTRATION NUMBER: 36,129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 12124 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.8
Best Local Similarity 100.
Matches 17; Conservative
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC INVENTION: DNA SEQUENCES AND USES THEREOF CORRESPONDENCE ADDRESS:
ADDRESSES: CIBA-GEIGY COFPORATION
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                             ö
                                                                                                                                                                     Ouery Match 6.8%; Score 17; DB 2; Length 12124; Best Local Similarity 100.0%; Pred. No. 16; Matches 17; Conservative 0; Mismatches 0; Indels
ordanisM: Cucumis sativus
| INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
| IMMEDIATE SOURCE:
| CLONE: pBScucchrcht5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10532
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,262
FILING DATE: 31-MAY-1995
''ASSTRICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 15-JUL-1993
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA: NO 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36, Application US/08456262
Patent No. 5851766
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moyer, Mary B.
Neuhaus, Jean Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
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Alexander, Danny C.
                                                                                                                                                                                                                                                                             51 AAAAAATCAGAAAATAT 67
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: USA
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US-08-456-262-36/c
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APPLICANT: MOVET. MAIY B.

APPLICANT: WOMENTS. WOLD.

APPLICANT: REALISON, CELTER F.

APPLICANT: SELISON, CELTER F.

APPLICANT: SELISON, CELTER F.

APPLICANT: SELISON, CELTER F.

APPLICANT: SELISON, CELTER S.

APPLICANT: WARTON: CELTER S.

APPLICANTON WAR
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APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Ward, Eric R.
APPLICANT: Ward, Eric R.
APPLICANT: Walliams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES:
STRFFF
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0
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                                                                                                                                                                                                                                                                              ORGANISM: Cucumis sativus
INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEPHONE: (919)541-8689
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 12124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLGY: linear
MOLECULE TYPE: DNA (9enomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLIN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAPELICATION NUMBER: US/08/455,736
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-1994
APPLICATION NUMBER: US 08/093,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
                                                                                                                                                                                                                                                                                                                                                                                                            6.8%;
100.0%;
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APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 AAAAATCAGAAAATAT 67
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.8
Best Local Similarity 100.
Matches 17; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                         ; IMMEDIATE SOURCE;
; CLONE: pBScucchrcht5
US-08-456-240-36
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STATE: New York
COUNTRY: USA
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APPLICANT:
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APPLICANT: Harms, Christian
APPLICANT: Friedrich, Leslie
APPLICANT: Beck, James
APPLICANT: Beck, James
APPLICANT: Ward, Eric
TITLE OF INVENTION: INDUCIBLE HERBICIDE RESISTANCE
TORRESPONDENCE ADDRESS:
ADDRESSE: No. 5942662artis Corporation
STREET: 3054 Corwallis Road, P.O. Box 12257
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/971,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR ADDITION: 900
PRIOR ADDITION: 900
PRIOR APPLICATION DAMA:
APPLICATION NUMBER: US 08/457,364
FILING DAME: 31-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
FILING DAME: 13-JAN-1994
APPLICATION NUMBER: US 08/093,301
FILING DAME: 16-UUL-1993
APPLICATION NUMBER: US 07/937,197
FILING DAME: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DAME: 1-ARE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-EBB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 6-ERB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 1-DEC-1990
PRIOR APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION NUMBER: US 07/425,504
FILING DATE: 21-DEC-1990
PRIOR APPLICATION UMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 7-SEP-1990
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045 057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
                                Patent No. 5942662
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Cucumis sativus
) INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: pBScucchrcht5
US-08-455-736-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S-19825/P1/CGC 1727
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 6-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 20-OCT 1989
FILING DATE: 27-SEP-1991
APPLICATION NUMBER: US 07/425,504
FILING DATE: 27-SEP-1991
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-5EP-1990
RADD APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
RION APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: VALUE NUMBER: US 08/045,957
FILING DATE: LA-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: ALGORITOR SCOLE
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-198
TELECOMMUNICATION INTORMATION:
TELEPHONE: (919)541-8649
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 12124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-08-971-217-36/c
; Sequence 36, Application US/08971217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.8
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 AAAAAATCAGAAAATAT 67
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us-09-895-435-4.rni

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FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy.
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/D1V5/CONT
TELECOMMUNICATION NUMBER: S-19825/P1/CGC 1727/D1V5/CONT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NO: 36:
TELECOMMUNICATION NO: 36:
NERANDEMATION FOR SEQ ID NO: 36:
LENGHI: 12124 base pairs
TELECOMMUNICATION NO: 36:
SEQUENCE CHARACTERISTICS:
LENGHI: 12124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: DNA (genomic)
ORGANISM: CHOUMIS Sativus
NOLECULE TYPE: DNA (genomic)
ORGANISM: Sativus
INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
INDIVIDUAL SOURCE:
CLOUME: PESCUCCARCTES
CLOCAL SIMIlarity 100.0%; Pred, No. 16;
MACCHES 17; CONSERVATION O' Mismatches O; Indels O; Gaps
OY SI NAMARANCRAGAARATH 67

OY SI NAMARANCRAGAARATH 11002
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Search completed: February 13, 2003, 06:42:21 Job time : 89 secs

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February 13, 2003, 04:56:57 ; Search time 114 Seconds
(without alignments)
1112.470 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                         1 ggggtaccgccagcatttcg......gacgcggaggaaatcacatg 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cgm2_6/ptodata1/pubpna/US07_puBCOMB.seq:*
(cgn2_6/ptodata1/pubpna/US07_NEW_PUB.seq:*
(cgn2_6/ptodata1/pubpna/US06_NEW_PUB.seq:*
(cgn2_6/ptodata1/pubpna/US06_PUBCOMB.seq:*
(cgn2_6/ptodata1/pubpna/US06_PUBCOMB.seq:*
(cgn2_6/ptodata1/pubpna/US08_NEW_PUB.seq:*
(cgn2_6/ptodata1/pubpna/US08_NEW_PUB.seq:*
(cgn2_6/ptodata1/pubpna/US08_NEW_PUB.seq:*
(cgn2_6/ptodata1/pubpna/US08_PUBCOMB.seq:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424239 seqs, 254661826 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_NA:*
                                                                                                                      nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                     OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                 US-09-895-435-4
                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                      OM nucleic -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
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Sequence 5, Appli Sequence 8, Appli Sequence 6, Appli Sequence 5, Appli Sequence 2720, Ap Sequence 441, Ap Sequence 4002, Ap Sequence 4002, Ap Sequence 121, Appli Sequence 11246, Ap Sequence 517, Appli Sequence 269, Appli Sequence 269, Appli Sequence 269, Appli Sequence 2816, Ap Description 0 US-09-838-718A-5 0 US-09-838-718A-8 0 US-09-838-718A-8 0 US-09-838-718A-6 0 US-09-070-927A-535 0 US-09-950-352-2720 0 US-09-938-842A-4602 0 US-09-938-842A-4602 0 US-09-938-842A-4602 0 US-09-938-842A-402 0 US-09-918-512-3 0 US-09-962-436-517 0 US-09-962-436-517 0 US-09-962-436-517 0 US-09-966-373-1246 0 US-09-966-373-1246 0 US-09-966-373-1246 0 US-09-966-373-1246 0 US-09-9676-889-269 DB Query Match Length 1500 2000 4704 116592 640681 Score

,	Sequence 102	Sequence 96 April	Section of App.	Socioso 71 Appli	Sequence /T/ Appl.	Sequence 3756, Ap	Seguence 1719, Ap	Sequence 101 App	Sections 1300	Section 124 April	, 0 7 6		7 -		ກໍ	'n		σ	Segmence 3 April 6	,,,	Section 110 An	9	2 0		2002		Sequence 9705, Ap	000	Sequence 503, App	
	US-10-098-841-192	US-09-070-927A-96	US-09-884-001-1	US-09-967-552A-71	75-6-16-16-16-16-16-16-16-16-16-16-16-16-1	10 00 104 017 1110	05-09-764-847-1719	US-10-098-841-101	US-09-764-868-1308	US-09-954-531-124	US-09-954-531-348	US-09-880-107-1590	US-09-967-768A-119	115-09-816-685-3	10-00-816-00E-2	03 03 010 011 011	9-908-500-07-50	US-10-003-806-9	US-09-822-246-3	US-10-113-877-174	US-09-974-300-4140	US-09-783-590-16	US-09-964-824A-69	US-09-960-352-13603	10-00-047-760-00-01	10 00 001 101 0101	90/6-T0/-/98-60-50	US-09-796-692-7000	US-09-983-965-503	
	σ	10	σ	10	1	9 6	7	ת	σ	σ	0	10	10	10	2	9 6	7 7	12	10	6	10	10	10	10	10	9 6	2	27	10	
	2389	2531	4610	4735	5676	0 10	000	64/3	11057	18596	18596	18596	18596	41104	94916	00000	70007	180557	197997	22	222	250	257	301	328	0 9 6	0 0	381	391	
	6.8	6.8	6.8	9.8	9.8	9		0	9.8	6.8	6.8	6.8	6.8	6.8	9	9 0		9.8	9.8	6.4	6.4	6.4	6.4	6.4	6.4			٠. 4	6.4	
	17	17	17	17	17	17	- F	/	17	17	17	17	17	17	17	17	1 -	7,	17	16	16	16	16	16	16	9 -) (o T	16	
	20	21	22	23	24	25	2 0	2 1	27	28	29	30	31	32	33	3.4		n (36	37	ω 	39	40	41	42	4.3		* !	45	
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ALIGNMENTS

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Sequence 5, Application US/09838718A

Sequence 5, Application US/09838718A

Sequence 5, Application US/09838718A

Setent No. US2002001904341

Setent No. US2002001904341

APPLICANT: Steidler, Lothar

APPLICANT: Steidler, Lothar

APPLICANT: Remaut, Erik R.

APPLICANT: Remaut, Erik R.

TITLE OF INVENTION: USE OF A CYTOKINE-PRODUCING LACTOCOCCUS STRAIN TO TREAT COLITI

CURRENT APPLICATION NUMBER: US/09/838,718A

CURRENT FILING DATE: 2001-04-19

PRIOR APPLICATION NUMBER: EP 98203529.7

PRIOR FILING DATE: 1998-10-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.1

SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTREX1 US-09-838-718A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 5230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.3%; Score 38; DB 10; 100.0%; Pred. No. 2.5e-09; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGGTACCGCCAGCATTTCGGAAAAAACCACGCTAAG 38
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 38; Conserv
RESULT 1
US-09-838-718A-5/c
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 5230
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RESULT 2
US-09-838-718A-7/c
; Sequence 7, Application US/09838718A
; Patent No. US20020019043A1
; GENERAL INFORMATION:
; APPLICANT: Steidler, Lothar
; APPLICANT: Remaut, Erik R.

US-09-938-842A-2876 US-09-938-842A-3160

439 1029 2000 2000

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Gaps

; 0

Indels

DB 10; L 2.5e-09; thes 0;

Length 5906;

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Steven Barash TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: plamsid pT1NX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATINE SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-MAY-2000
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DD 2999 GGGGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAG 2962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTR: USA
ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAG 38
CURRENT APPLICATION NUMBER: US/09/838,718A
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: PCT/PEP9/07800
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 8
SCOTHWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 5906
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
15.3%; Score 38; DB
Best Local Similarity 100.0%; Pred. No. 2.5
Matches 38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INCRAMATION:
NAME: Kenley K. HOOVER
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 535:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-070-927A-535
; Sequence 535, Application US/09070927A
; Sequence 535, Application US/09070927A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1566 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 535
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-070-927A-535
                                                                                                                                                                                                                                                                                                                                                              US-09-838-718A-6
                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
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| Sequence 8, Application US/09838718A
| Patent No. US20020019043A1
| Patent No. US20020019043A1
| Patent No. US20020019043A1
| Patent No. US20020019043A1
| APPLICANT: Steadut, Erik R.
| APPLICANT: Flers, Walter R.
| APPLICANT: Flers, Walter R.
| TILLE OF INVENTION: USE OF A CYTOKINE-PRODUCING LACTOCOCCUS STRAIN TO TREAT COLITIS
| FILE REFERENCE: 2676-4779US
| CURRENT FILING DATE: 2001-04-19
| PRIOR FILING DATE: 1999-10-06
| PRIOR FILING DATE: 1999-10-06
| PRIOR FILING DATE: 1999-10-20
| PRIOR FILING DATE: 1999-10-20
| PRIOR FILING DATE: 1998-10-20
| PRIOR FILING DATE: 1998-10-30
| SOFTWARE: PatentIn version 3.1
| SEQI DN 08 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Steidler, Lothar
APPLICANT: Remaut, Elik R.
APPLICANT: Fiers, Walter R.
TITLE OF INVENTION: USE OF A CYTOKINE-PRODUCING LACTOCOCCUS STRAIN TO TREAT COLITIS
FILE REFERENCE: 2676-4779US
APPLICANT: Fiers, Walter R.
TITLE OF INVENTION: USE OF A CYTOKINE-PRODUCING LACTOCOCCUS STRAIN TO TREAT COLITIS
FILE REFERENCE: 2676-4779US
CURRENT APPLICATION NUMBER: US/09/838,718A
CURRENT FILING DATE: 1001-04-19
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VESTOR 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTIMIL10 US-09-838-718A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.3%; Score 38; DB 10;
100.0%; Pred. No. 2.5e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
15.3%; Score 38; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2863 GGGTACCGCCAGCATTTCGGAAAAAACCACGCTAAG 2826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.39
Best Local Similarity 100.0
Matches 38; Conservative
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US-09-838-718A-6/c
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                                                                                                                                                                                                                                                                                                            SEQ ID NO 7
LENGTH: 5770
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US-09-38 842A-4541

Sequence 4541, Application US/09938842A

Sequence 4541, Application US/09938B42A

APPLICANT: Harper, Joel

APPLICANT: Harper, Joel

APPLICANT: Wang Xun

APPLICANT: AND TONG

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION UNMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR APPLICATION NUMBER: US 60/200,111

PRIOR APPLICATION NUMBER: US 60/200,111

PRIOR APPLICATION NUMBER: US 60/300,111

SEQ ID NO 4541

LENGANISM: Arabidopsis thaliana

US-09-938-842A-4541
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N: EXPRESSED IN BT474, SIGNAL = 0.61

N: EXPRESSED IN BONE MARROW, SIGNAL = 0.96

N: EXPRESSED IN HBLJOO, SIGNAL = 0.71

N: EXPRESSED IN PLACENTA, SIGNAL = 0.78

N: EXPRESSED IN PLACENTA, SIGNAL = 0.78

N: EXPRESSED IN PLACENTA, SIGNAL = 0.91

N: EXPRESSED IN LUNG, SIGNAL = 1.1

N: EXPRESSED IN HEAA, SIGNAL = 1.1

N: EXPRESSED IN HEAA, SIGNAL = 1.2

N: EXPRESSED IN HEAAT, SIGNAL = 0.99
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PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILICATION NUMBER: PCT/US01/00663
PRIOR PILICATION NUMBER: PCT/US01/00661
PRIOR PILICATION NUMBER: PCT/US01/00661
PRIOR PILICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILICATION NUMBER: PCT/US01/00661
PRIOR PILICATION NUMBER: US 60/234,687
PRIOR PILICATION NUMBER: US 60/234,687
PRIOR PILICATION NUMBER: US 09/608,408
PRIOR PILICATION NUMBER: US 09/608,408
PRIOR PILICATION NUMBER: US 09/774,203
PRIOR PILICATION NUMBER: US 00.000-05-05
PRIOR PILIC
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.2%; Sc. 100.0%; Pre 0;
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ORGANISM: HOMO SADIENS
FEATURE:
OTHER INFORMATION: MAP TO ACOOT
OTHER INFORMATION: EXPRESSED IN
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Best Local Similarity
Matches 18; Conservat
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR STITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FILE REFERENCE: Aconica x. 1.
CURRENT APPLICATION NUMBER: US 60/180, 312
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-26
PRIOR PELING DATE: 2000-06-36
PRIOR PELING DATE: 2000-09-3
PRIOR PELING DATE: 2000-09-37
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 2720
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; OGGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 12-LIB34-013-Q1-E1-C7
US-09-960-352-2720
                                       DB 10;
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100.0%; Pred. No. 12;
ive 0; Mismatches 0
                                                                                                              Mismatches
                                   7.6%; Score 19;
100.0%; Pred. No.
:ive 0; Mismatc
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Best Local Similarity 100.(
Matches 18; Conservative
                                                                                                          Conservative
                                   Query Match
Best Local Similarity
Matches 19; Conserve
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Sequence 517, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
    APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
                                                                                                GENERAL INFORMATION:
APPLICANT: BEASLEY. Ellen et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TILLE REPERENCE: CLOO1192
CURRENT APPLICATION NUMBER: US/09/818,512
CURRENT FILING DAIE: 2001-03-28
NUMBER: OF SEQ ID NOS: 4
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 3
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GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDBMI
APPLICANT: WATANABE, HIDBMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: GENOME DIA OF BACTERIAL SYMBIONT OF APHIDS ...
ITILE OF INVENTION: GENOME DIA OF BACTERIAL SYMBIONT OF APHIDS ...
FILE REFERENCE: 081356/0159
CURRENT FILING DATE: 2001-02-23
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN OF 2.1
SOFTWARE: PATENTIN OF 2.1
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Mismatches
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.2%; Score 18;
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LOCATION: (1)...(116592)

COTHER INFORMATION: n = A,T,C or G

US-09-818-512-3
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100.08; PIN
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                                                       ; Sequence 3, Application US/09818512; Patent No. US20020142416A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.2%; Sco
Best Local Similarity 100.0%; Pi
Matches 18; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA; ORGANISM: Buchnera sp. US-09-790-988-1
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-962-436-517/c
                                                                                                                                                                                                                                                                                                                                               LENGTH: 116592
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US-09-790-988-1/c
                                  US-09-818-512-3
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Sequence 4002, Application US/09938842A
Factor No. US20020160378A1
Factor No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Mang, Xun
TILE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPIANO 3
FURRENT FILING DATE: 2001-08-24
FRIOR FILING DATE: 2000-08-24
FRIOR FILING DATE: 2000-08-24
FRIOR FILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-06-22
FRIOR FILING DATE: 2001-06-22
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Sequence 3292, Application US/09764877

Patent No. US20020147140a1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT APPLICATION OF SEQ. 1001-01-17

Prior application data removed - refer to PALM or file wrapper;

NUMBER OF SEQ. ID NOS: 4031

SEQ. ID NO 3292

LENGTH: 4704
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             DB 9; Length 1500;
12;
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                                                           0; Indels
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red. No. 13;
Mismatches 0;
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                                                           Mismatches
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Pred. No.
                  Score 18;
7.2%; SCOL.
100.0%; Pre
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US-09-938-842A-4002
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                                    Best Local Similarity 100.
Matches 18; Conservative
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US-09-764-877-3292
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Best Local Similarity
Matches 18; Conserva
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US-09-938-842A-4002
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LENGTH: 2000
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Sequence 1356, Application US/09969373
GENERAL INCORMATION:
APPLICANT: Effertz. Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SRs and Methods of Genotyping
FILE REFERENCE: 38-10(55679)A
CURRENT ELLING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/756,427
PRIOR APPLICATION NUMBER: US 09/756,427
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 1246
LENGTH: 309
                                                                                                                                                                                                                                                                                 Query Match 6.8%; Score 17; DB 10; Length 148; Best Local Similarity 100.0%; Pred. No. 35; Matches 17; Conservative 0; Mismatches 0; Indels
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6.8%; Score 17; DB 10; Length 309;
Best Local Similarity 100.0%; Pred. No. 36;
Matches ·17; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001.09-25
PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR FILING DATE: 2000.09-25
PRIOR FILING DATE: 2000.09-25
PRIOR FILING DATE: 2000.09-25
NUMBER: OF SEQ ID NOS: 568
SEQ ID NO 517
LENTH: 148
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CORGANISM: Homo sapiens
US-09-962-436-517
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US-09-969-373-1246/c
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fzmb021f007c08 5', DNA sequence.
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Class: shotgun
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                BH781624.1 GI:19784825
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Best Local Similarity 100.
Matches 21; Conservative
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Salanoubat,M., Choisne,N., Artiguenave,F., Brottier,P., Wincker,P., Samson,D., Saurin,W., Weissenbach,J. and Quetier,F.
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Location/Qualifiers
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                                                                                        /organism="Homo sapiens"
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                      /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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8.8%; Score 22; DB 17; Length 796;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 22; Conservative 0; Mismatches 0; Indels
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/strain="Columbia"
/db_xref="texon:3702"
/clone="F4K3"
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         row: H column: 15
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/note="end : T7"
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AL082317
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           Plate: 3174 row
Seg primer: T7
Class: BAC ends
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; PaCC clade; Panicoideae; Andropogoneae; Zea.

21 (basea 1 to 561)

22 (basea 1 to 561)

33 Budiman, M.A., Freese, R.G., Bedell, J.A., Nunberg, A.N. and Lakey, N.D. Gendiman, M.A., Freese, R.G., Bedell, J.A., Ounberg, A.N. and Lakey, N.D. Contact: Bedell JA

Orion Genomics, LLC

4041 Forest Park Ave, St. Louis, MO 63108, USA

Tel: 314 615 6979

Fax: 314 615 5975

Email: jbedell@oriongenomics.com

Plate: ExabOllfO7 row: c column: 08
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LERIV03TR LERG Arabidopsis thaliana genomic clone LERIV03, DNA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 584)
Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T.,
Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
Genomic survey sequencing of Landsberg erecta ecotype of
Arabidopsis thaliana and identification of sequence-based
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Pred. No. 28;
0; Mismatches 0; Indels
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Unpublished (2000)
Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Location/Qualifiers
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100.0%; Pre
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8.4%; 5ccc. 100.0%; Pred. No. 2cc. 0; Mismatches
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/clone="PTB-153B07.F"
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100.0%; Pre
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R.Site 1 : SacI
R.Site 2 : SacI.
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Matches 21; Conservative
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BH860734
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/Grganism="Plasmodium berghei"
/Strain="ANKA clone 15cy1 (clone of the ANKA 8417 clone)"
/Glone_lib="Pb MBN #21"
/Clone_lib="Pb MBN #21"
/Glone_lib="Pb MBN #21"
/Gev_stage="asexwal blood forms"
/lab_host="Mus musculus"
/note="Vector: pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP: Site_l: EcoRV; Site_2: EcoRV; Genomic DNA was prepared from asynchronous blood stage forms of the cloned ANKA isolate of P. berghei grown in laboratory Swiss white mice. The DNA was purified from contaminating host DNA by Hoechst Dye 3328-CsCl ultracentifigation and precipitated Purified DNA was digested with mung bean nuclease in the presence of 36-38% formanide at 50 C, as described (Vernick, K.D., Imberski, R.B., and McCutchan, T.F. 1988 Nucleic Acids Research 16:6883-6896). The ends of the digestion fragments were polished using T4 DNA polymerase, and the fragments were polished using T4 DNA polymerase, and the fragments Skize selected in the range 500-2000 bp. These were ligated into the EcoRV-cleaved and dephosphorylated pBluescript SK(+) vector. Recombinant plasmids were used to transform E. coli XLIO-Gold host cells."
                                                    Location/Qualifiers

1. 584

7. Organism="Arabidopsis thaliana"

/Strain="Landsberg erecta"
/db_xref="taxon:3702"
/clone="LERIV03"
/clone="Inf="LeRG"
/note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.4-0.7 Kbp before ligation."

a 99 c 118 g 168 t
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266PbEll Pb MBN #21 Plasmodlum berghei genomic 3′, DNA sequence.
A2527276
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For additional information, see http://www.tigr.org/tdb/at/at.html
Seq primer: TR
Class: shotgun.
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Plasmodium berghei
Eukaryota; Alvoolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 588)
Carlton,J.M.-R. and Dame,J.B.
The Plasmodium vivax and P. berghei gene sequence tag projects
Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
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Fax: 352 392 9704
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Dept. of Pathobiology, College of Veterinary Medicine University of Florida
                                                                                                                                                                                                                                                                                                       Score 21; DB 17; Length 584;
Pred. No. 28;
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Seg primer: M13(-20) forward
Class: shotgun.
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1. .588
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Best Local Similarity 100.0%; Pr
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AZ527276/c
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218

BASE COUNT ORIGIN

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C bases 1 to 607)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission

Submitted (02-AuG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
17-22 Suehiro-chou, Tsurumi ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel.81-45-503-9111, Fax.81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-153B07.F.
Pan troglodytes
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                   Gaps
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BAC end sequences of Library PTB
Unpublished
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
a 41 c 142 g 187 t 21 others
DB 17; Length 588;
28;
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Pred. No. 27;
0; Mismatches 0; Indels
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KEYWORDS
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233 TCTTTTTTTATACAAAAAA 253

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="leaf"
/lab_host="leaf"
/lab_host="leaf"
/lab_host="leaf"
/lab_host="leaf"
/lab_host="leaf"
/note="Vector: pBeloBACII; Site_I: HindIII; Site_2:
HindIII; Ramets of P. trichocarpa (clone 383-2499) were
grown in the greenhouse. The trees were placed in the
dark for two days to deplete starch reserves prior to
harvesting approximately 60 g of fresh, young leaves.
Extraction of high molecular weight genomic DNA from leaf
nuclei was performed as described in Zhang et al. (1994).
Poplar genomic DNA was partially digested with HindIII
followed by three rounds of size selection from agarose
gels following separation by pulsed field gel electrophoresis (PFGE). In the first two size selections,
the pulsed field gel was run with a 90 second pulse at
160 V for a total run time of 18 hours at 110C. In both
runs DNA ranging from 200 kb to 400 kb was excised from
the gel and used in the next size selection. The final
size selection gel was run using a 6 second pulse at 150V
for 11 hours at 110C, and the compressed bank
was released from agarose by electroelution. The agarose
gel slice containing the >150 kb DNA was fragmented with
a razor blade and the resulting pieces placed in dialysis
bags (Gibco BRL, Rockville, MD). Electroelution was
carried out at 110C for 2 hours at 200 V followed by a second reversed-current pulse. Eluted DNA was quantified
by inspection on an agarose gel. HindIII-digested and
dephosphorylated pbelobBAC II (Shizuya et al. 1992) was
used for library construction. A molar ratio of
approximately 3:1 vector.insert was used for ligation.
Transformations were performed by electroporation using
Gene Hogs electrocompetent cells (Research Genetics,
Huntsville, AD) agar supplemented with 12.5 mg/ml
chloramphenicol and grown in 126 384-well microtiter
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Populus balsamifera subsp. trichocarpa.

Populus balsamifera subsp. trichocarpa

Bukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.

1 (bases: 1 to 756)

Striling, B., Yang, Z., Gunter, L., Tuskan, G. and Bradshaw, H.D.

Comparative sequence analysis between orthologous regions of the strabidopsis and Populus (poplar) genomes reveals substantial synteny and microcollinearity

Unpublished (2002)
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                                                                                                                                                                                                                                                                                             Contact: Stirling B
Department of Molecular Biology
Immunex Corporation
51 University Street, Seattle, WA 98101 USA
TH: 206 587 0430 ext. 54429
Email: StirlingB@Immunex.com
Insert Length: 726 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:3694"
/clone_lib="Poplar BAC Library"
/sex="female"
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Best Local Similarity
Matches 21; Conserv
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                                      ORGANISM
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AUTHORS
TITLE
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                SOURCE
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovidae; Bovidae; Bovidae; Boxidae; Boxidae;
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B10174 1180 bp DNA linear GSS 14-MAY-1997
F15G16-Sp6 IGF Arabidopsis thaliana genomic clone F15G16, DNA
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dept. of Biology, University of Pennsylvania, Philadelphia, PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: jecker@atgenome.bio.upenn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 20;
Mismatches
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University of Pennsylvania
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/clone="F15G16"
/clone_lib="IGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Columbia"
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100.0%; PIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Other_GSSs: F15G16-T7.1
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B10174.1 GI:2091293
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Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .1180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 215-898-9384
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100.0%; Pre
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Best Local Similarity 100.0%; Pr
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BI187613.1 GI:14661292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: broe@ou.edu
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Best Local Similarity
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                                                                         Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
FORWARD: AGGAAAAGCTATGACCAT
BACKWARD: GTTTCCAGTACAACGAC
Plate: 22 row: D column: 4
Seq primer: ATTTAGGTGACATAAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 19-APR-2001
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kukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Librarry made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary." 42.c 30 9 63 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cC-esflcLEL7K03al Tomato flower library from a mixture of developmental stages Lycopersicon esculentum cDNA clone CC-esflcLEL7K03al, mRNA sequence.
BG631395. GI:13682869
EST.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Lycopersicon esculentum"
/cultivar="165203"
/db_xref="taxon:4081"
/clone="cc-esflctEL7K03a1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lycopersicon.

1 (bases 1 to 277)
van dereneven.R.S.
ESTS from a tomato flower library
Unpublished (2001)
Contact: Rutger S. van der Hoeven
Cornell University
252 Emerson Hall, Ithaca, NY 14850, USA
Fax: 607 255 7886
Fax: 607 255 6883
Email: rv19@cornell.edu
                                                                                                                                                                                                                                                                                                                                                     1. .191
/organism="Bos taurus"
/db_xef="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 prime sequence.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 TTTTTTATACAAAAATAA 163
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Matches 20; Conservative
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ORIGIN
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VERSION
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BG631395
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       TITLE
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Hypocreales; mitosporic Hypocreales; Fusarium.

1 (bases 1 to 31)
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Other_ESTS: blb01fs.rl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
G20 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 68 5.5 gi|13376187|ref|NP_0 hypothetical protein FLJ23554
/clone_lib="Tomato flower library from a mixture of developmental stages"
/tissue_type="developing flower buds and open flowers" /dev.stage="developing flower buds and open flowers" /lab_host="XLOLR"
/note="Vector: pBK_CWN, Site_l: EcoRI; Site_2: XhoI; /note="Vector: pBK_CWN, Site_l: EcoRI; Site_2: XhoI; Flowers and flower buds were collected from greenhouse grown plants and used for library construction (cLEL).

47 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI187613 331 bp mRNA linear EST 10-JUL-blb01fs.fl Fusarium sporotrichioides Tri 10 overexpressed CDNA library Fusarium sporotrichioides CDNA clone blb01fs 3', mRNA
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Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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                                                                                                                                                                                                                                                                                                                                                     Length 277;
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/organism="Fusarium sporotrichioides"
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High quality sequence stop: 318.
Location/Qualifiers
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/clone="blb01fs"
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us-09-895-435-4.rst

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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence.
AQ058794
                                                                                                                                                                                                                            [Homosapiens
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Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusarium sporotrichioides.
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
I (bases 1 to 411)
Ren, Q., Taga, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, A. and Roe, B.
Analysis of a Fusarium sporotrichioides EST database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 10-JUL-2001
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                                                                         EST 30-JUL-2001
                                                                                                                                                                                                                                                                  Casas, E.,
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 353) Eathrenkrug,S.C.; Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                     Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith FPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Sus scrofa"
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/lab_host="pooled"
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Library made from pooled tissue from testis, ovary,
library made from pooled tissue from testis, ovary,
80 c 98 g 95 t
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12f05fs.fl Fusarium sporotrichioides Tri 10 overexpressed cDNA
ibrary Fusarium sporotrichioides cDNA clone j2f05fs 3', mRNA
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                                                                          31345004 353 bp mRNA linear 373681 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.0%; Score 20; DB 13;
100.0%; Pred. No. 1e+02;
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Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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100.0%; Pi
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BI191005.1 GI:14664684
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Best Local Similarity 100.
Matches 20; Conservative
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Sus scrofa
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                                     RESULT 12
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SM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 420)
S ddams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
L Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Tri 10"
/db_xraf="taxon:5514"
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cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript side end of cDNA cloned into XhoI site of pBluescript" side of S g 112 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html class: BAC ends.
                                                                                                                                                                                                                                                                                          Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 71 3.6 gi|13376187|ref|NP_0 hypothetical protein FLJ23554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mdadams@tigr.org Clones are derived from the human BAC library RPCI-11. For BAC
Unpublished (2001)
Other_ESTs: j2f05fs.rl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Blochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
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Pred. No. 93;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13-20
High quality sequence stop: 313.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
Mu, I (bases 1 to 462)

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Hu, G., Gu, J., Chen, Z. and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SoLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV682443 GKB Homo sapiens cDNA clone GKBADAll 5', mRNA sequence: AV682443 GKB CHOMO Sapiens CDNA clone GKBADAll 5', mRNA sequence: AV682443.1 GI:10284306
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/clone="RPCI-11-52A23"
/clone="RPCI-11"
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/cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Wector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
a 84 c 63 g 151 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: harzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="GKBADA11"
/db_xref="GDB:7519606"
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                                                                                                                                                                                                                                                                                                                        146 GTGTTATAATAAATA 165
                                                                                                                                                                                                                                                                                                                                               340 GTGTTATAATAAATATAAAT 321
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Search completed: February 13, 2003, 06:30:44

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Mismatches

DB 10; Length 462; 88; Indels

Score 20; Pred. No.

Query Match 8.0%; Soc Best Local Similarity 100.0%; Pr Matches 20; Conservative 0;

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Job time : 2292 secs

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